

7/185

31/11
 TCG CCG GCT CGC GGA CGT AGA TAA TAG CTC ACC GTT GGA CGA CUT CGA CAG GGT CCT TTG
 ser pro ala arg gly arg arg OCH AMB leu thr val gly arg pro arg gln gly pro leu
 61/21 31/31
 TGA CTG CGG GCC TTG ACC CGG ACC ACA GAG TCG CGT CAT CGC CTA AGG CTA CGG TTC
 OPA leu pro gly leu thr arg thr thr glu ser gly his arg leu arg leu pro phe
 121/41 121/51
 TGA CCT CGG GTC CGT CGG CGC CGA CGA STG AGG GAG TCA TGT CTC AGG GGC CGC CGC CAC
 CGA pro gly val arg gly arg arg val arg gln ser cys leu arg ala his arg his
 181/61 211/71
 TCC CGT CGC CGG CAG TCT CGG CAT GTG CAG ATG ACT TCA CGG ACC TTG TTC STG TTG STG
 leu gly arg arg gln cys his val gln met thr pro arg ser leu phe val leu val
 241/81 271/91
 TCG TGG TTG CGA CGA CTT CGC GCT GGT GAG CGC ACC CGG CGT CGT GGC CGC CAT CGG
 ser trp leu arg arg leu gly ala gly glu arg thr arg arg arg arg ala ala his ala
 361/101
 GAT C
 asp

SEQ ID N° 3A

FIGURE 3A

32/11
 CGC CGG CTC CGG GAC GTC GRT AAT AGC TCA CGG TTG GAC GTC GAC AGG GTC CTT TGT
 arg arg leu ala asp val asp asn ser ser pro leu asp asp leu asp arg val leu cys
 62/21 92/31
 GAC TGG CGG GCT TGA CGG GGR CGA CGA CAA ATG CGG GTC ATG CGC TAA CGC TAC CGT TCT
 asp cys arg ala OPA arg gly arg pro gln ser arg val ile ala OCH gly tyr arg ser
 122/41 152/51
 GAC CTG CGG TGC GTG CGC CGC GAC GAG TGA CGG AGT CAA GTC TCA CGG CGC ACC CGG ACC
 asp leu gly cys val gly ala asp glu OPA gly ser his val ser gly pro thr ala thr
 182/61 212/71
 TCG ATG CGC CGC AGT GTC AGC ATG TGC AGA TGA CTC CGC GCA GCT TGT TCG TGT TGG TGT
 ser val ala gly ser val ser met cys arg OPA leu his ala ala cys ser cys trp cys
 242/81 272/91
 CGT GGT TGC GAC GAC TTG CGG CTC CTG AGC CGA CGA CGC CGC CGC GTC STG CGG CGC ATU CGG
 arg gly cys asp asp leu ala leu val ser ala pro ala gly val val pro arg met arg
 392/101
 ATC
 ilc

SEQ ID N° 3B

FIGURE 3B

8/185

33/11

GCC GGC TCG CGG ACG TAG ATA ATA GCT CAC CGT TGG AGC ACC TCG ACA GGG TCC TTT GTG
 ala gly ser arg thr AMB ile ile ala his arg trp thr thr ser thr gly ser phe val
 63/21 93/31
 ACT GCC GGG CTT GAC GCG GAC GAC AGA GTC GGG TCA TCG CCT AAG GCT ACC CCT GTC
 thr ala gly leu asp ala asp asp his arg val gly sec ser pro lys ala thr val leu
 123/41 193/51
 ACC TGG GGT GCG TGG CGG CGG ACG AGT GAG GCA TCC ATG TCT CAG CCC CCA CGG CCA CCT
 thr trp gly ala trp ala pro thr ser glu ala val met sec glu gly pro pro pro pro
 183/61 213/71
 CGG TCG CGG GCA GTG TCA GCA TGT GCA GAT GAC TCC ACC CAG CTT GTT CGT STT GGT GTC
 arg ser pro ala val ser ala cys ala asp asp ser thr glu leu val arg val gly val
 243/81 273/91
 GTG GTT GCG ACG ACT TGG CGG TGA GCG GAC CGG CGS GCG TGG TGC CGC GCA TGT GCA
 val val ala thr thr trp arg trp OPA ala his pro pro ala ser cys arg ala tyr gly

TC

SEQ ID N° 3C

FIGURE 3C

31/11

CCA ATT TTC CTT CGC GCG GTG CAA TAC GAT CGT CAA GAC CGC CGA CGG CGG GTC GTT GCG
 pro ile phe leu arg ala val glu tyr his leu glu asp glu asp arg pro val val ala
 61/21 91/31
 GTC GCG CGG CTT CGG GAA ACC GCG TAT GGA CGC TGC TGT AGC GTT GTT GCG ACT TGA TGT
 val ala glu leu ala glu thr gly tyr gly pro cys arg thr val val ala thr GFA cys
 121/41 151/51
 CGT CGU TGT GCA CGG GTC CGG CGG CGA RAG GCA TTC CGA CAC TGG GAT CCT CAA AAC GTC
 arg arg ser pro pro val glu gly cys arg lys his asp exp pro glu asn val
 181/61 211/71
 GGC TGA GTG TGT GCA GGG CTC CGG GGA GCA GGC GAT CAT CAC CAT GTC CGA ACT GAA TAA
 gly OEA val ser ala gly leu arg gly ala ala asp his his val arg thr glu CGH
 241/81 271/91
 GTC CGC CGG CGA CTT CCA GAC ATT TGT TGT GGT TGC GGT TGA GGC CGA CGG GAG GCT
 val pro arg ala arg leu pro asp ile cys cys gly phe gly OPA gly arg gly glu ala
 301/101 331/111
 CAT TTC GCA CGA ACC GGT CTC CGG GTC GCA GGA TCG TTG CGG CGA TGG CGG CGC ACT GTC
 his phe ala ala thr gly leu arg val ala ala ser leu arg arg ser arg arg ser arg
 361/171
 CGG ACG ACT GGT CGT CAM CGA CGA CGA TC
 arg thr ser arg ala arg pro arg

SEQ ID N° 4A

FIGURE 4A

9 / 195

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32/11
CAA TTT TCC TTC GCG CGG TGC AAT AGC ATC TGC AAG ACC ATC GAC GGC CGG TGG TTG CGG
glu phe ser phe ala pro cys amn thr ile cys lys thr ser asp gly pro trp leu arg
62/21 92/31

TCG CGC ACG TTG CGG AAA CGG GGT ATG GAC CCT GGC GTA CGG TTG TTG CCA CTT GAT GTC
ser arg ser leu arg lys pro gly met asp pro ala val pro leu pro leu asp val
122/41 152/51

GTC GCT CTC CAC CGC TCG CGG GGC GAA AGC CAT TGC GAC RCF GGG ATC CTC AAA ACG TOG
val ala leu his pro ser gly gly glu ser his sec asp thr gly ile leu lys thr ser
182/61 212/71

GCT GAG TGT CTG CAG GGC TCC CGG GAG CAG CGC ATG ATC ACC ATG TAC GAA CTG AAT AAC
ala glu cys leu gln gly ser gly glu glu pro ile ile thr met tyr glu leu asn lys
242/81 272/91

TCC CGC CGG CGC GAC TTC CAG ACA TTT GTT GTG GTR TCG CTF GAG GGC GAG CGC AGG CTC
ser pro ala arg asp phe glu thr phe val val val val glu ala glu ala arg leu
302/101 332/111

ATT TGC CAG CAA CGC GTC TCC CGG TCG CAG GAT GGT TGC GGC GAT CGC GGC GUA CTC GTC
ile ser glu glu pro val val ser gly ser glu his arg cys gly asp arg gly sis val val
362/121

GGG CGA GTC GTC GTC AAC GAC GAC GAT C
gly arg val val asn ASP HIS ASN

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SEQ ID N° 48

FIGURE 4B

AAT TTT UCT TCG CGC CGT GCA ATA CCA TCT GCA AGA CCA CGG AGG GCC CGT GGT TGC CGT
 ASN PHE PRO SER ARG ARG ALA ILE PRO SER ALA ARG PRO ALA THR ALA ARG GLY GLY CYS GLY
 63/21
 CGC GCA CCT TGC CGA ARG CGG GTR TCG ACC CTC CGG TAC CGT TGT TGC GAC TTG ATG TCG
 ARG ALA ALA CYS GLY ASN ARG VAL TEP THR LEU PRO TYR ARG CYS CYS HIS LYS MET SER
 123/41
 TCG CTC TCC ACC CGT CGG GGG GCG AAA GCC ATT CGG ACA CTG GGA TCC TCA AAA COT CGG
 SER LEU SER THR ARG ARG GLY ALA LYS ALA ILE PRO THR LEU GLY SER SER LYS ARG ARG
 183/61
 CTG AGT GTC TGC AGG GCT CCG GGG AGC AGC CGA TCA GCA TGT AGC AAC TGA ATA AGT
 ALA SER VAL CYS ARG ALA PRO GLY SER SER ARG SER SER PRO CYS THR ASN GPR ILE SER
 243/81
 CGG CGG CGG CGG ACT TCG AGA CAT TTG TTG TGT TTT CGG TTG AGC CGG AGG CGG CGG TCA
 GLY PRO ARG ALA THR SER ARG HIS LEU ILE TRP PHE ARG LEU ARG PRO ARG GLY SER
 343/101
 TTT CGC AMG AAC CGG TCT CGG CGT CGT GCA AGC ATC TTG CGG CGG ATG CGG CGG CGG TCG TCG
 GLY ARG SER ASN ARG SER PRO GLY ARG SER SER ILE VAL ALA ALA ILE ALA GLY SER SER
 363/121
 GAG GAG TCG TCG TCA AGC AGG AGG ATC
 ASP GLU SER SER SER THR THR THR GLU

SEQ 13 N° 45

FEUILLE DE REMPLACEMENT (RÈGLE 26)

40 / 185

partie de la séquence nucléotidique de sondes

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1/1          31/13
CGG CGC GCG ACT TCC AGA CAT TTG TTC TGG TTT CGG TTS AGG CCG ARG CCA GGC TGA TTT
pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly ser phe
61/21          51/31
CGC AGC AAG CGG TCT CGG GGT CGG AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG TGG GAC
arg ser lys arg ser pro gly arg ser ile val ala ala ala ala ala gln ser ser asp
121/41
GAG TGG TCG TCA AGC ACC AGG ATC
gln ser ser ser the the thr ile

```

SEARCHED

FIGURE 4A³

1/1 31/31
CGC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT CAT TTC
arg ala arg leu pro asp ile cys cys gly phe gly GBA gly arg gly glu ala his phe
31/21 31/31
GCA GCA AGC GGT CTC CGG GTC GCA GCA TGG TTG CGG CGA TGG CGG CGC AGT CGT CGG AGG
ala ala ser gly leu arg val ala ala ser leu arg arg ser arg ser arg arg thi
121/41
AGT CGT CGT CAA CGA CGC CGA TC
ser arg ser ala arg arg arg

SEQ ID N° 481

FIGURE 4P-1

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L/1           31/11
GCC GCG TCC GAC TTC CAG ACA TTT GTT CTG GTT TGC GTC GAG GCG GAG AGG CTC ATT
ala ala arg asp phe glu thr phe val val val set val glu ala glu als arg leu ile
S/1/21          91/31
TCC GAG CAA GCG GTC TCC CGG TCG CAS CAT CGT TGC GGC GAT GCG GCG GCA GTC GTC GGA
ser gln gln ala val ser gly ser gln his arg cys gly asp arg gly ala val val gln
I/21/41
CGA GTC GTC GTC AAC GAC CAC GAT C
AGC val val val asp asp his asp

```

S2O₄²⁻/N⁺-SC₆H₅

FIGURE 4C'

11/185

ORF d'après par Cole et al. (Nature 393:537-544) et contenant la séquence Seq 4A'

1/1
 31/ii
 tga ata agt ccg ccg ggc act tcc aca cat ttg ttg tgg ttt cgg ttg agg ccg agg
 GCA ile ser pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg
 61/21 91/31
 cga ggc tca ttg ccg aag aag tct cgg ggt cgc aca aca gtt gcg gcg atc gcg gcg
 arg gly ser phe arg ser lys arg ecc pro gly arg ser ile val ala ala ile ala ala
 121/41 151/51
 cag tcc tgg gag tcc tgg tcc aca acc acy atc tcc gag tcc tgg aca ccc tcc tgt tcc
 gln ser ser arg glu ser ser thr thr thr ile ser asn ser thr pro ser cys ser
 181/61 211/71
 egg atc cta ccg aca cag ccg tcc atg gtg cgg ccc tgg ttc tac atc ggg atg ccc acc
 arg met leu arg arg gln arg ser met val ala pro leu leu tyr ile gly met his thr
 241/81 271/91
 gag atc aca ggt ttc gcc ggg tcc acc gag acc acc ttt gag gca tca cca ggg acc aca
 glu ile ser gly phe ala gly phe thr asp thr thr leu asp ala ser pro gly thr thr
 301/101
 tgg cga ctc aca gac tag
 trp arg leu arg asp AMB

SEQ ID N° 4F

FIGURE 4F

séquence en amont de seq4A' et en fusion avec seq4A'

1/1
 31/ii
 GCA ACC TAC CAG CAG AGC CAG CAG CGG CCT AAC CGA CCT AAA CGA GIA CGG CCC ATG AGT GAT
 ala thr tyr gln gln ser gln gly leu thr gly pro lys gly val ala pro met ala asp
 C

SEQ ID N° 4J

FIGURE 4J

seq4J' dans une autre phase de lecture

1/1
 31/ii
 ACG CAA CCT ACC AGC AGA GGC AGG GGC TCA CAG GAC CTA TAA GAG TAG TAG CGC CGA TGG CCT
 thr gln pro thr ser arg ala arg gly ser gln asp leu lys gln AMB arg pro trp leu
 61/21
 ATC
 ile

SEQ ID N° 4K

FIGURE 4K

seq 4J' dans la troisième phase de lecture

1/1
 31/ii
 CGC AGC CTA CGA CGA GAG CCA CGG CCT CGC AGG ACT TAA AGG ACT AGG CGC CCT CGC TGA
 arg san leu pro ala gln pro gly ala his arg thr CGH arg ser ser ala his gly GCA
 TC

SEQ ID N° 4L

FIGURE 4L

FEUILLE DE REMPLACEMENT (RÈGLE 28)

12/185

sequence Rv2050 prédicté par Cole et al. (Nature 393:537-544) et contenant seq43
 1/1 31/11
 ATG GCT GAT CTT CTC CGC AGG GGC ACT CGC CTC GGA CGC TCC GTG AGC TAT GAG ACC GAC GCG
 Met ala asp arg val leu arg gly ser arg leu gly ala val ser tyr glu thr asp arg
 61/21 61/31
 AAC GAA GAC CTC CGC CGC CGC CAG ATC GCA CGG TAC CGC ACC GAC AAC GGC GAG GAG TTC
 asp his asp leu ala pro arg gly ile ala arg tyr arg thr asp asn gly glu glu phe
 121/41 131/51
 GAA GTC CGC TTC CGC GAT GAC GCC GAG ATC CCC GGG ACC TGG TTG TGC CGC AAC GGC ATG
 glu val pro phe ala asp asp ala glu ile pro gly thy trp leu cys arg asn gly met
 181/61 211/71
 GAA GGC ACC CTG ATC GAG GGC GAC CTG CGC CAG CGG AAC AAG GTT AAG CGG CGC CGC ACC
 glu gly thy leu ile glu gly asp leu pro glu pro lys lys val lys pro phe arg thr
 241/81 271/91
 CAC TGG GRC AGC CTG CTG GAC CGC CGT TCC ATC GAA GAA GAG TTA CTT AAG GAG
 his trp asp met leu leu glu arg arg ser ile glu glu leu glu glt leu leu lys glu
 361/101 391/111
 CGC CTC GAG CTC ATT CGG TCA CGT CGG CGC GGC TGA
 arg leu glu leu ile arg ser arg arg gly DPA

SEQ ID N° 4M

FIGURE 4M

ORF d'après par Cole et al. (Nature 393:537-544) et contenant la séquence Rv2050
 1/1 31/11
 TAG TGC GGC CGG GAG TCC GAT CGC CGT ATC ATT GAT GGT CGG CGC CGC CGC GTC CGC CGC TGC
 AMB ser ala arg val ser asp pro gly ile ala asp gly arg ala ala arg val ala cys
 61/21 61/31
 CGG GAA CTA CGC AGA CGG CGG CAG CGT TTS CGA ATC GGA GGC ACT CGC CAG TAC GCA ACC
 arg glu leu arg arg arg pro gly arg leu pro tyr gly ala ser arg GAG tyt ala thr
 121/41 151/51
 TAC CAG CAG AGC CCA CGG CTC ACA GGA CCT ATA GUA GFA GCA CGC CGC ATC CCT GAT GAT CGT GTC
 tyr gly ser pro gly leu thr gly pro gly val ala pro met ala asp arg val
 181/61 211/71
 CGT AGG GGC ACT CGC CTC GGA CGC CGT AGG ATC GAC ACC GAG CGC CGC AAC CAC GAC CGT CGC
 leu arg gly ser arg leu gly ala val ser tyr ala thr asp arg ser his asp leu ala
 241/81 271/91
 CGG CGC CAG ATC CGG CGG TAC CGC ACC GAG AAC CGC GAG GAG GAG TTC GAA GTC CGG TTC CGC
 pro arg glu ile ala arg tyr arg thr asp ser gly alu glu phe glu val pro phe ala
 361/101 391/111
 GAT GAC CGC CGG ATC CGC CGC ACC TGG TTT TCC CGC AAC GGC ATG GAA GGC ACC CGT ATC
 asp asp ala glu ile pro gly thr tyr leu lys arg asp gly met glu gly thr leu ile
 421/121 451/131
 GAG GGC GAC CTC CGC CGG CGG AAG AAG GTT AAC CGG CGC CGG ACC CGC TGG GAC ATG CTC
 glu gly asp leu pro glu pro lys lys val lys pro pro arg thr his trp asp met leu
 481/141 511/151
 CTG GAG CGC CGT TCC ATC GAA GAA GTC GAA GAT TTA CTT AAC GAG CGC CGC CTC CGG CGC ATT
 leu glu arg arg ser ile glu glu leu glu leu lys glu arg leu glu leu ile
 541/161
 CGG TCA CGT CGG CGC CGC CGC TGA
 arg ser arg arg arg gly DPA

SEQ ID N° 4N

13/185

31/11

GAT CGG GGT CAA CGA GGC CGA ATA CGG CGA GAT GTG GGC CGA AGA CGC CGC CGC GAT GTT
 asp arg gly gln arg gly arg lle arg arg esp val gly pro esp arg arg arg esp val
 61/21 91/31

TGG CTA CGC CGC GGC GAC GGC GAC GAC GGC GAC GTT GCT GGC GTT CGA GGA GGC GGC
 trp ien arg arg gly esp gly esp gly esp val als als val arg gly gly ala
 121/41 151/51

GGA GAT GAC CGG CGC GGC TGG GCT CCT CGA CGA GCA GGC CGC CGC GGT CGA GGA GGC CTC CGA
 gly esp esp gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg
 181/61 211/71

CAC CGC CGC GGC GAA CGA GTT GAT GAA CAA TGT GCG CGA GGC GCT GCA ACA GCT GGC CGA
 his arg arg gly glu pro val arg glu gln cyc ala pro gly als als thr als gly pro
 241/81 271/91

GCC CAA CGA GGG CAC CAC CGC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GGT CTC CGC
 als his als gly his his als phe phe gln als gly trp pro val gly esp gly leu als
 301/101

GCA TCG GTC CGC GAT C
 ala ser val als esp

SEQ ID N° 5A

FIGURE 5A

32/11

ATC CGG CTC ACG GAG GGC GAA TAC CGG GAA GAG ATG TTG CGG CAA GAC CGC CGC CGG ATG TTT
 ile als val asn glu als glu tyr gly glu met trp als gln esp als als als met phe
 62/21 92/31

GCG TAG CGC CGG ACG CGC ACG CGG ACG GCG ACG TTG CTG CGG TTC GAS GAG CGG CGG
 gly tyr als als als als thr als thr als als thr als als als als als als als pro
 122/41 152/51

GAG ATG ACC AAC CGG GGT GGG CTC CTC GAG CAG CGC CGC GCG GTC GAG GAS GAG CGC TCC GAC
 glu met thr ser als gly gly leu leu gln gln als als als val glu glu als ser esp
 182/61 212/71

ACC CGC GCG GCG AAC CAG TTG ATG AAC AAT GTC CGG CGC CGG CTC CAR CAG CTC CGC CGC CAG
 thr als als als asn gln leu met asn asn val pro gln als leu gln gln leu als gln
 242/81 272/91

GCC ACG CAG CGG ACC ACG CCT TCT TCC AAG CTG GGT CGC CGC CTC TGG AAG ACC GTC TCG CGN
 pro thr gln gly thr thr pro ser ser lys leu gln gln leu trp lys thr val ser pro
 302/101

CAT CGG TCG CGG ATC
 his arg ser pro ile

SEQ ID N° 5B

FIGURE 5B

14 / 185

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33/11
TGG CGG TCA ACG AGG CGG AAT ACG GCG AGA TGT GGG CCC AAG ACG CCG CGG CGA TGT TTG
ser arg ser thr arg pro asn thr ala arg cys gly pro lys thr pro pro arg cys leu
63/21                                         53/31
GCT ACG CGG CGG CGA CGG CGG CGG CGA CGT TGC TGC CCT TCG AGG AGG CGC CGG
ala thr pro arg arg arg arg cys cys cys arg ser arg arg arg arg arg arg arg
123/41                                         153/51
AGA TGA CCA GCG CGG GTG GGC TCC TCC ACG AGG CGG CGG CGG TCG AGG AGG CCT CGG ACA
arg OPA pro ala arg val gly ser ser arg pro pre arg ser arg arg pro pro thr
183/61                                         213/71
CCG CGG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC ARC AGC TGG CGG AGC
pro pro arg arg thr ser OPA OPA the met cys pro arg arg cys asn ser tri phe ser
243/81                                         273/91
CCA CGC AGG GCA CCA CGC CTT CTT CCA AGC TGG GTG GGC TGT GGA AGA CGG TGT CGG CGG
pro arg arg ala pro arg leu leu pro ser trip val ala cys gly arg arg ser arg arg
303/101
ATC GGT CGC CGA TC
ile gly arg arg

```

SEQ ID N° SC

FIGURE 5C

sequence substitution see [seq](#)

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1/1 31/11
CGC CGG GCT GAC GGC GAC GGC GAC GAC GTC GCT GGC GTT CCA GCA GGC GGC GGA GAT
arg arg gly asp gly asp gly asp gly asp val ala ala ala val arg gly gly ala gly asp
81/21 91/31
GAC CAG CCT CGG TGG CCT CCT CGA CGA GGC GGC CCC GGT CCA GGA GGC CTC CGA CAC CGC
asp gln arg gly tpp ala pro arg ala gly arg arg gly arg gly gly leu arg his arg
121/41 151/51
CGC GGG GAA CCA GTT GAT GAA CAA TGT GGC CCA GGC GCT GCA ACA GCT GUC CCA GCG CAC
arg gly glu pro Val asp glu gln cys ala gly ala ala thr ala gly pro ala his
181/61 271/71
GCA GGG CAC CAC GCC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GCT CTC GGC GCA GTC
ala gly his his ala phe phe gln ala gly tpp pro val gln asp gly leu ala ala ser
241/81
GTC GCT GAT c
val ala est

```

SEQ ID N° 5A

FIGURE 5A-1

25/185

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1/1          31/31
TAC GCG GCG GCG ACG CGG AGC GCG AGC TGT CTG CCG TTC GAG GAG GCG GCG GAG
tyr ala ala ala thr ala thr ala thr leu leu pro phe glu glu ala pro glu
61/21
ATG ACC AGC CGG GGT GGG CTC CTC GAG CAG GGC GCC GCG GTC GAG GAG GGC TCC GAC ACC
met thr ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp thr
121/41
GCG GCG AAC CAG TTG ATG AAC ATC ATG CCC CAG GCG CTG CAA CAG CTG GGC CAG CCC
ala ala ala asn gln leu met asn asn val pro glu ala leu glu gln leu ala gln pro
181/61
ACG CAG GGC ACC ACG CCT TCT TCG AAG CTC GGT GGU CTG TCG AAG ACC GTC TCG CCC GAT
thr gln gly thr the pro ser ser lys leu gln gly gly leu trp lys thr val ser pro his
241/81
CGG TCG CGG ATC
arg ser pro ile

```

SEQ ID N° 58

FIGURE 35 m

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1/1          31/11
ACG CGG CGG CGA CGG CGA CGG CGA CGG CGA CGT TGC TGC CGT TCG AGG AGG CGC CGG AGA
thr pro arg arg arg arg arg arg arg cys asp ser arg arg arg arg asp arg
61/21          51/51

TGA CCA CGG CGG GTC GGC TCC TCG AGC AGG CGG CGG CGG TGC AGG AGG CGT CGG ACA CGG
OPA pro ala arg val gly ser ser ser big pro pro arg ser arg arg arg pro pro thr pro
121/41          151/51

CGG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC AAC AGC AGG TGG CCC AGG CGA
pro arg arg the ser OPA OPA thr met cys pro pro arg cys asn ser trp pro ser pro
181/61          211/71

CGC AGG GCA CGA CGG CTT CTT CGA AGC TGG GTG GCT TGT GGA AGA CGG TGT EGC CGC ATC
arg arg ala pro arg leu leu pro ser trp val ala cys gly arg arg ser ser arg arg ile
241/81

GCT CGG CGA TC
gly arg arg

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USC ID: M³ 303

FIGURE 5C

16/185

ORF prédicté par Cole et al. (Nature 393:537-544) et contenant seq5A'

1/1 31/11
tga act gat gat tct gat agc gac caa act ttt gca aca aac ccc ggc gat ccc ggt
OPA thr asp asp ser asp ser asp gln pro leu gly ala lys his pro gly asp arg gly
61/21 91/31
caa cgg ggc cga ata cgg cga cat gtc ggc cca aca cgc cgg cgc gat gtt tgg ata cgg
gln arg gly arg ile arg arg asp val gly pro arg arg arg asp val trp leu arg
121/41 151/51
mgc ggc gac ggc gac gtc gac gtc gtc gtc gtc gtc gca gga ggc gcc gga gtc gac
arg gly asp gly asp gly asp val ala ala val arg gly gly ala gly asp asp
181/61 211/71
cgg cgc ggg tgg gct cct cga gca ggc cgc cgg ggt cga ggs ggc ctc cga ccc cgc cgc
gln arg gly trp ala pro arg ala gly arg arg gly gly leu arg his arg arg
241/81 271/91
ggc gac cca gtt gat gaa caa tgt gtc cca ggc gtc gca aca gtc ggc ccc gcc ccc gca
gly glu pro val asp gln gln cys ala pro gly ala ala thr ala gly pro ala his ala
301/101 331/111
ggc ccc ccc gcc ttc ttc ccc gct ggg tgg cct gtc gca gac ggt ctc gcc gca tcc gtc
gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala ala ser val
361/121 391/131
gac gat gag cca cat ggt gtc gat ggc cas cas cca cat gtc gat gag cca ccc egg tgg
ala asp gln his gly val asp gly gln gln pro his val asp asp gln leu gly cys
421/141 451/151
gtc gat gag cca cac ctt gag ctc gat gtt gaa ggg ctt tgg tcc ggc ggc ggc ccc cca
val asp asp gln his leu glu leu asp val glu gly leu cys ser gly gly arg arg pro
481/161 511/171
ggc cgg gca aat nco ggc gca aas cgg ggt acc gtc gat gac ccc gtc gtc ggg ccc ccc gtc
gly arg ala aia aia arg gly ala lys arg gly pcc gly asp gly leu ala gly gln leu ala
541/181 571/191
ggg ttc ttc ggg tct ggg cgg tgg ggt gac ccc ccc ggg tcc ggc ggc ccc gtc ggt egg
gly phe phe gly ser gly arg trp gly gly arg gln leu gly ser gly gly leu gly arg
601/201 631/211
ttc gtt gtc ggt gcc gca ggc ctg ggc cgg cgg gac gtc aac ccc ggg gec gec phe
phe val val gly ala ala gly leu gly aat aly gln pro gly ser his pro gly gly ala
661/221 691/231
ggc gct gcc gct gac ccc gac ccc gac ccc cgg cgg gtc gac gtc gtc gtc gtc gtc
gly ala ala ala asp gln pro asp gln arg arg gly lys arg ala asp ala asp ala gly
721/241 751/251
ggc gct gcc ggt egg gca gat egg cgg ccc cgg cgg tgg gtc gtc gtc gtc gtc gtc
arg ala ala ala gly ala asp gly arg gln gly arg arg trp trp ala gln trp cys ala ala
781/261 811/271
tgt tcc gcc ggg aac cta tgt gat gtc gca tcc tcc ggc ggc ccc ccc gga gac ggg ggc
cys ser ala ala ala thr leu cys asp ala ala phe ser gly gly arg leu gly glu gly ala
841/281
cag act gtc gtt att tgg
gln thr val val ile OPA

SEQ ID N° 5F

FIGURE 5F

17/185

séquence Rv1186 prédictée par Cole et al. (Nature 393:537-546) et pouvant coder pour une ORF en fusion avec Seq5A'

1/1

31/11

atg gtg gat ttg ggg gcg ttc cca ccg gag atc acc tcc ggc agg atg tac gcc ggc cgg
met val asp phe gly sia leu pro pro glu lls ssn ser ala arg met tyr ala gly phe
61/71

51/31

gtt tgg gac tcc ctg gtc gcu gcg gct cag atg tgg gag acc gtc gog agt gag ctg tt
gly ser als ser leu val als als gln met trp asp ser val als ser asp leu phe
121/41

151/51

tgg gcc gcg tcc ggg ttg cay tgg gty gtc gtt cag acc gtc ggc tgg tgg ats ggt
ser als als ser als phe gln ser val val trp gly leu the val gly ser trp lls gly
181/61

211/71

tcc tgg ggc ggt ctg atg gtg gcc gcg gcc tgg cog tat gtc ggc ggg atg acc gtc acc
ser ser als gly leu met val als
ala als ser pro tyr val als trp met ser val thr
241/81

271/91

gog ggg cag gcc gag ctg acc gcc gtc gat cgg gtc gct ggg ggg gtc tac gag agg
ala gly gin als glu leu thr als als gln val ser als als als als tyr glu thr
301/101

331/111

gcy tat egg ctg acc gtc ccc cog cog gtc gtc gtc gtc gtc gtc acc cgt gct gca ctg arg atc
ala tyr gly leu thr val phe pro pro val lls als gln ssn arg als gln leu met lls
361/121

391/131

ctg ats gcc acc acc ctc ttg ggg cca acc acc acc ggg acc acc ggg gtc acc acc ggg gca
lss als als thr aso leu leu gly gln asn phe als lls als val ssn glu als glu
421/141

451/151

tcg ggc gag atg tgg gco was gag gag gag atg tgg tcc gag tac gag gag gag gag
cys gly glu met trp als gln asp als als als met phe gly tyr als als als the als
581/161

511/171

acc ggg acc acc ttg ctg ccc ttg gag gag gag gag gag gag gag ats acc acc acc gag gag gag
thr als als thr als thr leu leu pro phe glu glu als pro glu met thr sss als gly gly
541/181

571/191

ctc acc gag gag gcc gag gtc gag gag gag gtc tcc gac acc gca gag gnc acc gag ttg
rea leu glu gln als als val glu als als ser amp thr als als als asn gln leu
601/201

631/211

atg acc eat gta ccc acc gag gtc cca ccc acc gag acc acc acc acc acc acc acc
met ann ann val pro gln als led gln gln leu als gln pro thr gln gly thr the pro
581/221

661/231

tct too eat ctg ggt ggc atg tgg tgg acc acc gtc tgg eat egg tgg tgg atc acc acc
ser ser lys als led gly leu trp lys the val ser pro his arg ser ser pro lls ser asn
721/241

751/251

atg tgg tgg atg gcc acc acc cao atg tgg ats ann acc tcc ggt gtc tgg tgg atg acc acc
met val ser met als als ann his met ser met the ann ser gly val ser met thr asn
781/251

811/271

acc ttg tgg atg atg ttg acc acc gtc tgg ttt gct acc ggg ggg ggg ggg ggg gtc tgg caa acc
thr leu ser ser met leu lys gly phe als pro als als als als gln als val gln the
841/281

871/291

ggc gcy caa acc ggg gtc ccc ggg ggg atg tgg ctg ggg acc tgg tgg atc acc acc
ala als gln als gly val als met ser sea leu gly ser swf leu gly ser ser gly
901/301

931/311

ctg ggg ggt ggg ttg gtc acc acc tgg gct acc ggg ggg ggg ggg gtc gtc gtc gtc tgg tgg tgg
leu gly gly gly val als als als asn leu gly arg als als als ser val gly ser leu ser val
961/321

991/331

tgg cay pcc tgg gcc gca acc
par gln als trp als als als asn gln als val thr pro als als arg als leu pro leu
1021/341

1051/351

acc
the ser leu the thr als als als gln als gly phe gly gln met leu gly gln pro val
1081/361

1111/371

agg maa atg ggc gdc agg ggg ggg ggt
gly gln met gly als arg als gln gln gly gln ser gly val leu arg val phe pro his
1141/381

1171/391

ucc tat gtc agg dog cat ttt tgg dog gtc gtc gtc tag
pro tyr val met pro his ser pro als als gly Arg

SEQ ID N° 5R

18/185

Seq 5P: ORF d'après Cole et al. (Nature 302:537-544) et contenant la séquence Rv186

1/ 31/13
tag ggc cac gta atg gty gat ttc egg gcg tta ccc cgg gag atc acc tcc ggg agg atg
AMG gly his val met val asp phe gly ala leu pro pro glu ile ser ser ala arg met
61/21 91/31
tac ggc ggc ccc ggt tag gcc tag ctg gtc gca ggg gct cag atg tgg gac aco ggg ggg
tyr ala gly pro gly ser ala ser leu val ala ala ala glu met trp asp ser val ala
121/41 151/51
tgt gac ctg ttt tac gcc gtc tag gtc ttt cag tcc ggg gtc egg ggt ctg acc gtc ggg
ser asp ien phe ser ala ala ser ala phe gln ser val trp gly leu thr val gly
181/61 211/71
tgt rgg ats ggt tag tag ggg ggt ctg atg gtc ggg ggg ggg ggg tag ccc ggg ggg
sec trp ile gly ser ser ala gly leu met val ala ala ala ser pro tyr val ala trp
241/81 271/91
atg aac gtc acc gca ggg cag gcc gag ctg acc gca ggg ggg ggg gtt gct ggg ggg
met ser val thr ala gly gln ala glu leu the ala ala gln val arg val ala ala ala
301/101 331/111
ggc tag gag acc ggg tag ggg ttt acc acc ccc ccc ccc ggg acc ggg acc ggg acc ccc
ala tyr glu thr ala tyr gly leu the val phe pro val ile ala glu amn arg ala
361/121 391/131
gaa ctg atg att ctg aca gca acc acc ccc ttc ggg caa sec acc ccc ggg ats ggg ggg
glu leu met ile ieu iie ala thr amn leu leu eiy gln sec thr pro ala ilc ala ynl
421/141 451/151
acc gag gca gaa tac ggc gag atg tag gct caa gag gca ggg ccc ccc atg ttt ggg tac gag
amn glu ala glu tyr gly glu met trp ala gln amn als ala ala met phe gly tyr ala
481/161 511/171
ccg ggg acc ggg acc ggg acc ggg acc acc ttc ctg ccg ttc ggg ggg ggg ccc gag atg acc
ala ala thr ala thr ala thr ala thr leu pro phe glu glu ala pro glu met thr
541/181 571/191
agg ggg ggt ggg acc ccc gag ccc ggg
ser ala gly gly leu leu glu gln ala ala val val glu glu ala ser esp thr ala ala
601/201 631/211
ggc acc ccc ttc ang acc eat gtg ccc caa gag ggg ccc ccc ccc acc acc acc
ala amn gln leu met amn amn val pro gln ala leu gln gln leu ala gln pro thr gln
661/221 691/231
ggc acc acc cat tat tcc acc acc ctg ggt egg ccc tgg aag acc acc gtc tcc ccc eat egg tgg
gly thr thr pro ser ser lys leu gly gln leu trp lys thr val ser pro his arg ser
721/241 751/251
ccg acc
pro ile ser amn met val ser met ala amn his met eek met met the acc ser gln val
781/261 811/271
ttc tag acc
ser met thr amn thr leu ser ser met leu gly lys gly lys ala pro ala ala ala gln
841/281 871/291
ggc dtg cca acc acc ggg ggg cca acc
ala val gln thr ala ala gln amn gly val arg ala met ser ser leu gly ser ser leu
901/301 931/311
ggg tcc tcc ggt acc
gly ser ser gly leu gly gly gly val ala ala amn leu gly arg ala ser val gly
961/321 991/331
ttc ttg tcc ggt acc
ser amn ser val pro ala trp ala ala ala amn gln ala val thr pro ala ala arg
1021/341 1051/351
ggc ccc acc
ala leu pro leu thr ser leu the ser ala ala gln arg ala pro gly gln met leu gly
1061/361 1111/371
ggc ccc acc
gly leu pro val gly gln met gly ala arg ala gly gly leu ser gly val leu arg
1141/381 1171/391
gtt acc
val pro phe arg pro pro tyr val met phe ser pro ala ala gly AMG

SEQ ID N° SP

19/185

31/11

GGA TCC TGA TGC AAG TGG TCC GGG ATT TGT CGG CAG CCA CGG CGG TCC CGT CGA CCA AGC
 gly aer DPA cys lys trp ser gly ile cys arg gls pro arg arg ser arg arg pro thr
 61/21

TTG GTG CAT CGG GCG TGC GAG CAT ACA CGC ACC GAC CAG CGC GGC GAG CGG CGG TAG CTG
 leu val his pro gly cys glu his ala arg thr asp gin arg gly glu arg gly AMB leu
 121/41

131/51

CTT GCC GAC TGT TCC TCC CTG CGG GCA CCA TGT GCG ACA AGC TTA AGC GCA GCA GTC CGG
 leu ala his cys ser ser leu pro ala pro cys ala thr ser leu ser ala ala val pro
 181/61

211/71

GCG GTG CCT GGG CAT CCA GCA AAA CGG GGA CCT CAA GAA CGA TTC ATG AAC GAG GGG TCC
 ala val pro gly his pro ala lys arg gly ala glu arg phe met asn glu gly sec
 241/81

271/91

TCA CCA AGC TCG AAA CGG AGC GTT GCC AGC CGG CGC AGC ATA TTA CGT GCT CGA CGG TCC
 ser pro thr ser lys pro thr val ala ser arg pro thr ile leu arg ala arg gly ser
 301/101

331/111

GCT GTR CCC TCA CGG AAC GTG ACT CCT ACA CGG CGG AGC CGG ACT CTG GGG TCG TTA
 ala val pro ser pro asn val ser pro thr pro arg arg ala ttr leu ala ser leu
 361/121

391/131

GCA CGC GAG CTC AGG GTG TCC CGC AGC ATG GTC TCG AGT GCT TTT AAC CGA CGG GAT CGA
 ala ala glu leu lys val ser arg thr thr val ser asn ala phe asn arg pze asp pro
 421/141

GAA CGA GAA GAT C
 glu gly glu asp

SEQ ID N° 6A

FIGURE 6A

32/11

GAT CCT GAT GCA ACT GGT CGG GGA TTT CTC GGC AGC GAC CGG GGT CGC GTC GAC CAA CGT
 asp pro asp ala ser gly pro gly phe val gly ser his gly gly pro val asp glu arg
 52/21

92/31

TGG TCC ATC CGG GCT CGG AGC ATG CAC GCA CGC ACT AGC GCG CGG AGC CGG CGT AGT TCC
 trp cys ile arg ala ala ser met his ala pro the set ala ala ser ala ala ser cys
 122/41

152/51

TTG CGC ACT GTT CCT CGC TGC CGG CAC CAT GCG CAA GGT TAA CGC CAG CGG TAC CGG
 leu pro thr val pro pro cys arg his val arg gln ala CGH ala gln qin Eyr arg
 182/61

212/71

CGG TGT CGT CGC ATG CGG CAA AAC CGG GAG CTC AAG AAC GAT TTA TGA AGG AGG GGT CGF
 arg cys leu gly ile gln qin asn gly qin leu asp ser OPA thr arg gly arg
 242/81

272/91

CAC CAA CGT CGA ATW CGA CGG TTG CGA GGC CGG CCA CGA TAT TGC GTC CTC GAG GGT CGG
 his gln arg arg asn arg arg leu pro ala gly pro arg tyr cys val leu glu gly pro
 302/101

332/111

CTG TAC CCT CAT CGA AGC TGA GTG CGC CAC CGC CGA CGG CGG CGA CTC TGG CGT CGT TAG
 leu tyr pro his arg thr OPA val pro his arg gly gly gly arg leu ttp arg arg ADH
 362/121

392/131

CGG CGG AGC TCA AGG TGT CGC GCA CGA CTG TCT CGA ATG CTT TTA AGC GAC CGG ATC CGT
 gln pro ser ser arg phe pro ala pro leu ser arg met leu leu thr asp arg lla gln
 422/141

AAG GAG AAG ATC
 lys glu lys lla

SEQ ID N° 6B

FIGURE 6B

FEUILLE DE REMPLACEMENT (REGLE 26)

20/185

33/11

ATC CTG ATG CAA GTG GTC CGG GAT TTG TCG GCA AGC CGG CTC CGG TCG AAC AAC GTT
 ile leu met gin val val arg asp leu ser ala ala thr ala val pro ser thr aia val
 63/21 93/31

GCT GCA TCC CGG CTC CGA GCA TGC ACG AAC CGA CGA CGG CGG CGA CGG CTA GCT GCT
 gly ala ser gly leu arg ala cys thr his arg pro ala arg arg ala arg leu ala ala
 123/41 153/51

TGC CCA CTG TTC CTC CCT GCC CGC ACC ATG TGC GAC AAG CTT AAC CGC AGC AGT AGC CGC
 cys pro leu phe leu pro ala gly thr met cys arg lys leu lys arg ser ser thr gly
 183/61 213/71

GGT GCC TGG GCA TCC AGC AAA AGC CGG AGC TCA AGA AGC ATT CAT GAA CGA CGG GCG GTC GTC
 gly ala trp ala ser ser lys thr gly ser ser arg thr ile his glu arg gly val val
 243/81 273/91

ACC AAC GTC GAA AGC GAC GGT TGC CAG CGC CGC AAC GAT ATT GCG TGC TCG AGG GTC CGC
 thr aia val glu thr asp gly cys glu pro ala his arg ile ala cys ser arg val arg
 303/101 333/111

TGT AGC CTC ACC GAA CGT GAG TCC CGC ACC CGC GAG GCG CGC GAC TCT GCG GTC GTT AGC
 cys the leu thr glu arg glu ser his thr ala glu ala gly asp ser gly val val ser
 363/121 393/131

AGC CGA CCT CAA GGT GTC TCG CAC CAC TGI CTC GAA TGC TTT TAA CGG ACC GGA TCC AGA
 ser arg ala glu gly val pro his his his cys leu glu cys phe DCH pro thr gly ser arg
 423/141

AGG AGA AGA TC
 arg arg arg

SEQ ID N° 6C

FIGURE 6C

31/11

CCG TCG GCA ACT TGG CGG CTC AGG TCG GCT TGA TCC CTC CGG CGA GGC GGG TCA CGC ATT
 pro ser ala thr trp pro leu arg ser ala GAA ser leu gly arg gly gly ser ala ser
 61/21 91/31

AGC GGC TCC ATC CGG TTT GCT GGT AGC GCT TGG GGA AGC TAG CGG CGA CGT TGT CGG
 ser gly ser ile gly phe ala gly ser gly ser ala gly ser AMB arg arg arg cys arg
 121/41 151/51

TGG CCG GTG ATA TAT TCG GTC AGA CGG GTC TGG CGG CGG CGT AGG TGA TCT GCG AGA CGC
 trp pro val ile tyr trp val arg arg val trp arg arg leu arg DPA ser ala thr arg
 181/61 211/71

CSC CGC GGT GCT CGA GGC AGG CTT AGC ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT
 arg arg gly ala arg ala arg leu thr arg glu phe arg lys cys tyr ser glu his
 241/81 271/91

CTT GTA TCT CTT CTC CGT GCG ACC CGC TAG TGG TAG TGT TTT CGA GTC CGG GCA GAT CGT
 leu val ser leu leu arg ala thr pro AMB val AMB his phe arg val pro ala esp pro
 301/101

AGG TGG ACC AGG TCT CAG CAG ATC
 ame phe thr arg ser his glu ile

SEQ ID N° 7A

FIGURE 7A

21/185

32/11

CGT CGG CAA CTT GGC CGC TGA GGT CGG CTT GAT CCC TGG GTC AAG GCG GGT CAG CCA ATA
 arg arg gln leu gly arg gln leu asp pro trp ala glu ala gly gln pro ile
 62/21 62/31
 GCG GCT CCA TCG GGT TTA CTG CTA CGG GTT CGG CGG GAA GCT ACG GGC GAC GTT GTC GGT
 ala ala pro ser ala leu leu val ala val arg arg glu ala ser gly asp val val gly
 122/41 152/51
 CGC CGG TCA TAT ATT GGG TCA GAC CGG TAT GGC CGG CGC TGA GCT GAT GAT CTG CGA CGC CGC
 gly arg GFA tyr ile gly ser asp gly tyr gly gly gly GFA gly asp leu arg his ala
 182/61 212/71
 GCC GCG GTG CTC GAG CCA CGC TTA CGA CGA GGG AAT TTC GAA AAT GTT ATT CGG AAC ATC
 ala ala val leu glu pro gly leu arg pro gly asn phe glu asn val ile gln asn ile
 242/81 272/91
 TTG TAT CTC TTC TCG GTG CCA CGC CCT AGG TAT AGT GTT TTC GAG TAC CGG CAG ATC CGA
 leu tyr ied phe ser val pro pro pro arg cys ser val phe glu tyr arg gln ile pro
 362/101
 GGT TCA CGA CGT CTC ACC AGA TC
 gly ser pro gly leu thr arg

SEQ ID N° 7B

FIGURE 7B

33/11

GTC GGC AAC TTG CGC GCT GAG GTC CGC TTG ATC CCT CGG CGG AGG CGG GTC ACG CGA TAG
 val gly asn leu ala ala glu val gly leu ile pro gly pro arg arg val ser gln AMB
 63/21 63/31
 CGG CTC CAT CGG CTT TCG TGG TAG CGG TTG GGC GGG AAG CTA CGG CGG CGG AGG TTO TCG GTC
 arg leu his arg leu cys trp AMB arg phe gly gly lys leu ala ala thr leu ser val
 123/41 153/51
 GGC GGT GAT ATA TTG GGT CGG ACG CGT ATC CGG CGC GCT GAG GTC ATC TCG CGC ACG CGG
 ala gly asp ile leu gly gln thr gly met ala ala ala glu val ile cys asp the pro
 183/61 213/71
 CGG CGG TGC TCG AGC CGG CGT TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACR TCT
 pro arg cys ser ser gln ala tyr asp gln gly ile ser ser lys met leu phe arg thr ser
 243/81 273/91
 TGT ATC TCT TCT CGG TCG CAC CGC CTA GGT CTA GTG TTT TCG ACT ACC CGG AGA TCC CGG
 cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser gln
 303/101
 GTT CAC CAG GTC TCA CGA GAT C
 val his gln val ser pro asp

SEQ ID N° 7C

FIGURE 7C

22/185

31/11
 CTT TGC GTG ATG TCC AAT GGC GAA ANC GAC GGC TTG TCA TCG TCA GCA CGG GGC
 leu cys val met ser asp gly glu asn asp ala ieu ser ser gln ser ser als pro ala
 61/21
 51/31
 TAG TTT TCG CGA TGA CGC TCG TTC TGA CGC GAC TTG TGA AGC GGT TTC CGG TCG AGG CGG
 AMB phe ser arg CPA arg ser phe CPA pro asp leu CPA thr gly phe gly ser arg pro
 121/41
 151/51
 AGC GAA CGG TCG ATT CCA TGG GTG TCG ACG CAT TGG TCG TCA AAG CGG GCG CGG CAG GAC
 ser glu pro ser ile pro trp val ser thr his ser trp ser arg pro als arg gln asp
 161/61
 211/71
 CGT TCG TGG GTT CGA AAC CAT TCG CCC AAA TCG ACC TCG CGG ACG TTG CTC GTG CGG CGG
 arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val arg leu
 241/81
 271/91
 GCG TCT TGG CTG CGG CGC CGC CAC TAG CGA CTC CGC CGT CGA CGA TCC CGC CGC AGG GCA CGT CAG
 als ser trp leu pro pro his AMB arg leu arg arg arg ser gly arg als arg gln
 301/101
 331/111
 CGC TCA CGG CTC CGG CAG CAG ACG ACG GAC CGG CGA TGC CGC CGG GGG TCT CGG
 arg gln thr ser pro arg ser gly his gln ser tns esp pro als cys arg gly ser arg
 361/121
 391/131
 AGC GTC CGG CGC CAT CGA CGC CGG ACG ACG TGG CGG TGT CGA CGA CGC CGC TGG CGG GAA ACC
 thr val gly arg his arg arg arg thr arg ser arg cys arg als arg trp als glt thr
 421/141
 TCG CGG AGC ANC
 ser als thr ile

SEQ ID N° 8A

FIGURE 8A

32/11
 TTT CGG TGA TGT CCA ATG GCG AAA ACG ACG CCT TGT CAT CGC AAT GGT CAG CAC CGG CGT
 phe ala CPA cys pro met ala lys thr thr pro arg his arg ASN arg gln his arg pro
 62/21
 52/31
 AGT TTT CGG GAT GAC GCT CGT TGT GAC CGG ACT TGT GAA CGG GGT TCG GGT CGA CGC CGA
 ser phe arg arg asp als arg ser asp arg the cys glu arg val ser gln arg arg gly arg
 122/41
 152/51
 CGG AAC CGT CGA TTC CAT CGG TGT CGA CGC ATT CGT CGA CGG CGG CGC CGC CGC AGG ACC
 als ASN arg arg phe his gly cys arg arg ile arg gly gln gly arg arg gly arg thr
 182/61
 212/71
 CGT CCT CGG TTC GAC ACC ATT CGG CGA AAT CGA CCT CGC CGA GGT TGC TCG TCG CGC CGC TGG
 val pro gly phe esp thr ile arg pro ASN arg pro als pro gly cys ser cys als tpp
 242/81
 272/91
 CGT CTT CGG TCG CGC CGC ACT ACG GAC TGC CGC CGC CGC GAT CGG CGA CGG CGC CGC CGC ACC
 arg leu gly cys arg pro thr ser esp cys als val esp esp pro als gly his val ser
 302/101
 332/111
 GCG AAA CCT CGC CGG GGT CGG CGT ACC AGA CGA CGG ACC CGG CAT CGC CGG CGG GGT CGC CGA
 ala lys ASN his arg val arg gly thr arg als arg thr arg his als als gly leu gly
 362/121
 392/131
 CGG TCG CGG CGC ATG GAC CGG CGA CGA CGT CGC GGT CGC GGT CGC CGG CGG AAA CCT
 arg ser gly als ile asp als gly arg gly arg gly val als his als gly pro lys pro
 422/141
 CGG CGA CGA TC
 arg arg arg

SEQ ID N° 8B

FEUILLE DE REMPLACEMENT (REGLE 26)

23/385

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33/11
TTG CGT GAT GTC CAA TGG CGA AAA CGA CGC CTT GTC ATC GCA ATC GTC AGC ACC GGC CTA
leu arg asp val gln trp arg lys arg arg leu val ile als ile val ser thr gly leu
63/21                                         93/31

577 TTC GGG ATG ACC CTC GTT CTG ACC GGA CTT GTC AAC GGG TTT CGG ATC GAG GGC GAC
val phe als met thr leu val ile thr gly leu val asn gly phe arg val gln als gln
123/41                                         153/51

CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC GTC AAG GCC GGC GCG GCA GGA CGG
arg thr val asp ser met gly val asp als phe val val lys als gly als als gly pro
183/61                                         213/71

TTC CTC GGT TCG ACA CCA TTC GCT CAA ATC CCC CCC CGG GTT GCT CGT GGG CCT GCG
phe leu gly ser thr pro phe als gln ile asp leu pro gln val als arg als pro gly
243/81                                         273/91

GTC TTG GCT GCG CCA CTA GCG ACT GCG CCG TCG ACG ATC CGG CAG CCC AGC TCA GCG
phe leu als als als pro leu als thr als pro ser thr als arg gln gly thr ser als
303/101                                         333/111

CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CGC GGT ATG CGG CGG GTC TCG GAC
arg asn val thr als phe gly als pro glu his gly pro gly met pro arg val ser asp
385/121                                         415/131

GGT CGG GCG CCA TGG ACC CGG GAC GAG GTC GCG GTC TCG AGG AGC CGT GGC CMA AAC CTC
gly arg als pro ser thr pro asp glu val als val ser ser thr leu gly arg asn leu
423/141

GGC GAC GAT C
gly asp asp

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SEO ID N° 8C

FIGURE 8C

partie d'une séquence supplémentaire de secou-

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1/1          31/11
CAG GTT GGT CGT GCG CCT GGC GTC TTG GCT GCG CCA CTA GCG ACT GCG CGG TCG ACG
gin val als arg als pro gly val leu als ala pro leu als thr als pro ser thr
61/21
ATC CGG CAG GGC ACG TCA GCG CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC CGA CCC
ile arg gin gly thr ser als arg asn val thr als phe giv als pro glu his gly pro
121/41
GGC ATG CGG CGG GTC TTG GAC GGT CGG CGG TCA TCG ACC CGG GAC GAG GTC GGG GTC TTG
gly met pro arg val ser asp gly arg als pro ser thr pro asp glu val als val ser
181/51
AGC ACG CTG CGC CGA AAC CTC GGC GAC GAT C
ser thr leu gly arg asn leu gly asp asp

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00000000000000000000000000000000

FIGURE 8A *

24/185

1/1

31/11

AGG TTG CTG GTG CGC CTC GCG TCT TGG CTC CGG CCC AAC TAG CGA CTC CGG CGT CGA CGA
 arg leu leu val arg leu ala ser trp leu pro pro his AMB arg leu arg arg arg arg
 61/21 91/31

TCC GGC AGG GCA CGT CAG CGC GAA ACG TCA CGG CGT TCG CGG CAC CAG AGC AGC AGC GAC CGG
 ser gly arg ala arg gln arg thr ser pro arg ser gly his gln ser thr asp pro
 121/41 151/51

GCA TGG CGC CGG TCT CGG ACG CTC CGG CGC CAT CGA CGC CGG AGG TCG CGG TGT CGA
 ala cys arg gly ser arg thr val gly arg his arg arg arg thr arg ser arg cys arg
 181/61

GCA CGC TGG CGC GAA AGC TCG CGG ACG ATC
 ala arg trp ala glu thr ser ala thr ile

SEQ ID N° 8B'

FIGURE 8B'

Seq8C

1/1

31/11

CCA CGT TGC TGC TGC GGC TGG CCT CTT GGC TAC CGG CGC ACT AGC GAC TGG CGG GTC GAC
 pro gly cys ser cys ala trp arg leu gly cys arg pro thr ser asp cys ala val asp
 61/21 91/31

GAT CGG GCA CGG CAC GTC AGC CGG AAA CCT CAT CGG CGT CGG TGC ACC AGA GCA CGA CGG AGC
 asp pro ala gly his val ser ala lys arg his arg val arg arg gly thr arg ala arg thr
 121/41 151/51

CGG CAT CGC CGC CGT CTC GGA CGG TCG CGG CGC XTC CGT CGA CGA CGA CGT CGC CGT GTC
 arg his ala ala gly leu gly arg ser gly ala ile asp ala gly try gly arg gly val
 181/61

GAG CAC GCT CGG CGG AAA CCT CGG CGA CGA TC
 glu his ala gly pro lys pro arg arg arg

SEQ ID N° 8C'

FIGURE 8C'

25/185

équence RY2563 prédicté par Cole et al. (Nature 393:537-541) et contenant seq8A'

atg
met
121/41 151/51
ctt ttc ggc gtc ttg cgt gat gtc cca agg cga aca cgg ctc gtc atc gca atc gtc
leu phe ala als leu arg asp val gln trp arg lys arg arg leu val ile als ile val
181/61 211/71
agc acc ggc cxa gtt ttc gcg akg acg ctc gtc ctc agg gga ctt gtc aac cgg ttt cgg
ser thr gly leu val phe ala met thr leu val leu thr gly leu val asn gly phe arg
241/81 271/91
gtc gag gdc gaa gga acc gtc gat tcc atg ggt gtc gac gca ttc gtc gtc aac ccc ggc
val glu als glu arg thr val asp ser met gly val asp als phe val val val lys als gly
301/101 331/111
gag gca gga aac ttc ctt ggt tcc aca cca ttc gcc cca atc gac atc ccc dgg gtc gct
ala als gly pro phe leu gly ser thr pro phe als gln ile asp leu pro gln val als
361/121 391/131
cgt cgg ctc ggc gtc tgg gtc gct gca cta ggc act ggc cgg tcc acg atc cgg cag
arg als pro gly Val als als als pro leu als thr als pro ser thr ile arg gln
421/141 451/151
ggt aac tca gug tgg aac gtc acc ggc tcc ggg gca cca ggg gac gca ccc ggc atc cgg
gly thr ser als arg arg val thr als phe als pro gly his gly pro gly met pco
481/161 511/171
agg gtc tcc gao ggt cgg gca ccc tgg acg ccc gag gag gtc tcc agc acg atc
arg val ser asp gly arg als pro ser thr pro asp gly val als val ser ser thr leu
541/181 571/191
ggc cgg aac ctc ggc gac gat ctg cca ctg ggt ggc cgg aac ttc cgg atc gtc ggc atc
gly arg asn leu gly asp asp leu gln val gly als arg thr leu arg ile val gly ile
601/201 631/211
ggc ccc gag tca acc ggg ctg gca aag att ccc aac atc ttc ctt cgg aac aac gaa ggc cta
val pro glu ser thr als leu als lys ile pro aac als phe leu thr thr gly leu
661/221 691/231
cag cgg tcc gca tac aac gpa cag ccc aca atc aat tcc atc ggg atc gtc ggg arg ccc
glu gln leu als tyr asu gly gln pro thr ile ser ser ile gly ile asp gly met pro
721/241 751/251
cgg ccc ctc ccc gac ggc tat cag acc gtc aat cca tcc gat ggt gtc aac gat ccc gtc
arg gln leu pro asp gly tyr gln thr val asn arg als asp als val ser asp ile met
781/261 811/271
cgg ccc tcc aag gca ggg gty gat gca atc acg gtt gtc ggg gtc ttc cgg aac gtt
arg pro leu lys val als val asp als ile the val val als val leu leu trp ile val
841/281 871/291
ggc gag tcc ato gtc ggc tcc gtc gtc atc tcc tcc ggg ttc ggg ggg ctc cgg aac ttt
als als leu als val gly ser val val tyc leu ser als leu gln arg leu arg asp phe
901/301 931/311
gog gtg ttc aag ggg aac ggc gtc ccc acg cgg atc ctc gtc gtc gca ccc ggg ccc
ala val phe lys als ile gly val pro thr ser ile leu als gly leu als leu gln
961/321 991/331
gog gtc gtc gtc gac ctc ttc gca ggg ccc gtc ggc aac ctc tcc ccc ccc ccc
als val val val als leu als als val val gly ile ile leu ser als leu ile
1021/341 1051/351
ccc ttc tcc ccc atg aac gtc gtc gtc ccc ctc aat gtc gtc gtc gac gca ccc ggg aac
pro leu phe pro met the val val val pro leu ser als phe val als leu pro als ile
1081/361 1111/371
ggc acc gtc atc ggt ctc ctg ccc akg aac gtc gca aya ctc cgg ccc gtc gtc gtc gtc
ser thr val ile gly leu leu als als ser val als gly leu arg arg val val als ile asp
1141/381
ccg gca atc gcc ttc gga ggt aac tcc
als als leu als phe gly gly pro AMB

SEQ ID N° 80

26/185

ORF prédicté par Cole et al. (Nature 363:537-544) et contenant RV2563

1/1

31/11

tag gtt tea aya agg oct qtg cag gtt tcc gca gcc tgg gcc cog cog cca cog aag aco
AMS val ser arg arg pro val ser ser ala ala trp ala ala ala pro pro lys ser
61/21 91/31ccg cog aat tgg gct aat cgy gtc cgc ttg gct cga tgg ccg arg aco tgg acc gca acc
pro pro lys ala ala arg val arg leu ala ala ser pro met ala ser thr ala thr
121/41 131/51acc gag ccc ccc acc tcc qtc gac acc ccc cgg cca acc ccg gca aco cca gca cat gat
thr asp pro leu thr ser val glu pro arg arg the asn ala ala thr pro ala his asp
181/61 211/71cat ttg aat tgg tcc acy gaa gca ggt aca ttc cgg ccc aat ctt ttt gug gct ttg cog
his leu ile gly ser thr glu ala gly ser phe arg arg met leu phe ala ala leu arg
241/81 271/91cat gtc cca aat tgg cga aca cca cgg ccc ttg gtc acc gtc acc acc ggc cta qtt rto
asp val ala trp arg lys arg leu val the ala ile val ser thr gly ileu val phe
301/101 331/111gcg atg acc ccc gtt ctg acc gga ccc ttt gac aat ggg ttt cgg gco gag gtc qag bga acc
ala met thr leu val leu the gly leu val ala gly phe arg val glu ala glu arg the
361/121 391/131gtc gat tcc atg ugt gtc gac gca ttc qtc gtc sag acc ggc gco gag gtc qag bga acc
val asp ser met gly val asp ala phe val val lys ala gly ala ala gly pro phe leu
421/141 451/151tgt tcg aca cca ttc gct cca atc gac ctg cod eaq gtc gct gtc cog cgt ggg acc ggc gtc tcg
gly ser thr pro phe ala glu ile asp leu pro glu val ala arg ala pro gly val leu
481/161 511/171gtc gag gca cca cta gag act gac acc tcc aco acc acc acc acc acc acc acc acc acc
ala ala ala pro leu ala thr ala pro ser thr gly arg gly ala ala arg acc
551/181 581/191gtc acc ggc ttc ggg gca cca gag acc gga ccc ggc arg ccg ccg gtc tcc gac egt cog
val thr ala phe gly ala pro glu his gly pro gly met pro arg val ser asp gly arg
661/201 691/211gng cca tcg acc cgg gag gac gtc gug tcg aeg aco ctg gpp cca acc ccc ggc gag
ala pro ser thr pro asp glu val ala val ser ser thr leu gly arg asn leu gly asp
661/221 691/231gtc ctc cca ggg ggt pgg cgg acc ttg cgg aco gtc ggn acc gtt acc ggg tca acc ggg
asp leu val val gly ala arg the leu arg lle val gly the val pro glu ser thr ala
721/241 751/251ctc gca aag att ccc aad acc ttc ctg acc acc gca gac gtc ctc cag cag ttg gca tcc acc
leu ala lys the pro san ilo phe leu thr the glu ala leu gln ala leu ala tyr asp
781/261 811/271ggc ccc ccc acc acc agt tgg acc ggg acc gac ggg acc ggg acc acc acc acc acc acc
gly gly pro thr ilo ser ser ile gly ile asp gly met pro arg gln leu pro asp gly
841/281 871/291tat ccc acc acc acc cca ggg gat gtc gtc aco gtc acc gtc acc acc acc acc acc acc
tyr gln thr val asn arg ala asp ala val ser asp leu met arg pro leu lys val ala
901/301 931/311ctg gat gug acc acc gtc gtc ggg acc gtc acc gtc acc gtc acc gtc acc gtc acc gtc
val asp ala ile the val val ala val leu leu trp ile val ala ala leu ile val gly
951/321 981/331tgt gtc gtd ttc acc tcc tcc ggg acc gtc acc gtc acc gtc acc gtc acc gtc acc gtc
ser val val cyl leu ser ala leu glu arg leu arg asp phe ala val phe lys ala ile
1021/341 1051/351ggc gtt ccc acc
gly val pro thr arg ser ile leu ala gly leu ala leu gln ala val val ala leu
1081/361 1111/371ctc ggg ggg ggg gtt gtt gtt gtc acc ccc ccc ccc ccc ccc ccc ccc ccc
ile ala ala ala val val gly gly ile leu ser leu leu leu ala pro leu phe pro met thr
1141/381 1171/391gtc ggg gca acc
val val val pro leu ser ala phe val ala leu pro ala ile ala thr val ile gly ileu
1201/401 1231/411ctg gtc aag acc gtc
ile ala ser val ala ser ala gly ileu arg arg val val ala ile asp pro ala leu ala phe gly
1261/421

tgt cod tag

gly pro AMS

SEQ ID N° 8F

FEUILLE DE REMPLACEMENT (RÈGLE 26)

27/185

séquence de Rv0072 prédicté par par Cole et al. (Nature 393:537-544) et présentant plus de 77% de similarité avec SeqSD'

1/1 31/11
 atg ctc ttc gcg gcc ctc cgt gac atg cca tgg aag aac ead cgc ctc gtc gtc atc aac atc
 Met leu phe ala ala leu aag asp met gli trp arg lys arg arg leu val ile thr ile
 61/21 91/31
 atc aac acc egg ctc atc ttc egg atg aac ott qtt ttt acc gga ccc ggc aac ggc ttc
 ile ser thr gly leu ile phe gli met thr leu val leu thr gly leu ala aac gli phe
 121/41 151/51
 cgg gtg gag gaa egg cac acc gtc gat tcc atg ggt gtc gat gta itc gtc gtc aca tcc
 arg val gli ala arg his thr val asp ser met gli val asp val phe val val arg ser
 181/61 211/71
 ggc gct get gga cct trt ctc ggt bca atc ccc ttt ccc gat gtt gat ctc gcc cca gtc
 gly ala ala gli pro phe leu gly ser ile pro phe pro asp val asp leu ala arg val
 241/81 271/91
 gcc got gaa ccc egg ggt atg gcc gog gac ccg tgg ggc aca gtc ggg acc atc atg aca
 aie ali gli pro gli val met ala ala ala pro leu gli ser val gli thr ile met lys
 301/101 331/111
 gaa ggc acc tcc acg cga sac gtc acc gtc ttc ggc ggg ccc gag cac gga sac ggc atg
 glu gly thr ser thr arg aca val thr val phe gli ala pro gli his gli pro gli met
 361/121 391/131
 cca cgg gtc tca gag ggt cgg tca ccc tcc aac ccc gac gaa gtc gag gca ttc aca acc
 pro arg val ser gli gli arg ser pro ser lys pro asp gli val ala ala ser ser thr
 421/141 451/151
 atg ggc cca cac ctc ggt gac act gtc gac gtc gtc ggg ccc aca ttc ccc gtc gtt ggc
 met gli arg his leu gli asp thr val gli val gli ala arg arg leu arg val val gli
 481/161 511/171
 att gtc ccc aat tcc acc gca ctc gac aac ccc aat gtc ttc ccc aac acc gac ggc
 ile val phe ser ser the ala leu ala lys ile pro ser val phe leu thr the gli gly
 541/181 571/191
 ttg caa aat ttc gcy tac aac ggg cag ccc aat aac ctc att ggg atc atc aat gtc aat arg
 leu gli lys leu ala tyr asp gli gli pro asp ala the ser ile gli ile gli met
 601/201 631/211
 ccc cga cay ctc ccc gag ggt tac caa aat ttc gag ccc ggt gyc get gtc aat gat trp
 pro arg gli leu pro gli gly tyr gli the phe asp arg val gli ala val aac asp leu
 661/221 691/231
 gtc ccc cca ttg aag gtc gca gty aat tcc aat ccc aat ggg gtc gtt ttc ctc tcc ggg att
 val arg pro leu lys val ala val aac ser ile ser ile val ala val leu leu trp ile
 721/241 751/251
 gtc ggg gtc ctc aac gtc ggc tcc gtc gtc gtc att ccc tcc tcc gtc get ott gag cgg ctc ctc cgt gac
 val ala val leu ile val gli ser val val tyr leu ser ala leu gli arg leu arg asp
 781/261 811/271
 ttc ggg gtc ctc aac gtc ggc tcc gtc gtc gtc att ccc tcc tcc gtc get ott gag cgg ctc ctc cgt gac
 phe ala val phe lys ala ile gli thr pro thr arg ser ile met ala gli leu ala leu
 841/281 871/291
 ccc ggc ctc gtc att ccc tcc gtc ggg gtc
 gli aia leu val ile ala leu leu ala ala val voi gli val val leu ala gli val leu
 901/301 931/311
 gca ccc ctc ccc aat aat gtc ggg gta ccc gtc ggt get tac ctc ggg ctc aac gtc
 ala pro leu phe pro met ile val ala val pro val gli ala tyr leu ala leu pro val
 961/321 991/331
 gcc ggg atc gtc aat gtc ggt wtc tcc gtc get aca gtc gtc ggg aac gtc
 aie ala ile val ile gli leu phe ala ser val ala gli leu lys arg val val thr val
 1021/341
 gat ccc ggg aag ggg tcc gga ggt ccc tag
 asp pro ala gli ala phe gli gli pro AMB

SEQ ID N° 8G

28/185

SeqSH : ORF prédicté par Cole et al. (Nature 333:537-544) et contenant seqSG
 1/1 31/11
 tag ctc ctg gga arg ccc ttc gcy gco ctg cgt gac atg aca tgg aya aag ccc cpc ctg
 AMB pro leu gly met leu phe ala ala leu arg asp met gln trp arg lys arg arg leu
 61/21 91/31
 gtc atc acc atc atc acc acc ggg ctg atc ttc ggg atg aca ctt gtt ttg acc gga ccc
 val lle thr ile ile ser thr gly leu lle phe gly met thr leu val lle thr gly leu
 121/41 151/51
 gcg acc ggc ttc cgg ggg gcc cgg cac acc gtc gat tcc atg ggt gtc gat gaa ttc
 ala asn gly phe arg val glu ala arg his thr val esp ser met gly val asp val phe
 181/61 211/71
 gtc gtc aca tcc ggc gct gct gga cct ttc ctg ggt tca aca ccc gat gat gac
 val val arg ser gly ala ala gly pro phe leu gly ser ile pro phe pro asp val esp
 241/81 271/91
 atg gcc cga gtc gac gat gaa ccc ggt gtc atg gcc ggc acc ccc ttg ggc aca gtc ggg
 leu ala arg val ala ala glu pro gly val met ala ala ala pro leu gly ser val gly
 301/101 331/111
 acg atc aty aca gaa ggc acg acg tcc acg aca aca gtc acc atc ttc ggc gca ccc gac
 thc lle met lys glu gly thr ser thr aca val met thr val phe gly ala pro glu his
 361/121 391/131
 gga cct ggc atg cca cgg gtc tca gag ggt egg tca aca tgg tcc aca ccc gac gaa gtc ggg
 gly pro gly met pro arg val ser gly arg ser pro ser lys pro asp gly val ala
 421/141 451/151
 gca tcg aca acg atg ggc cga acc ctc ggt gac act gtc ggg gtc ggg cgg aca aga ttg
 sia ser ser thr met gly arg his leu gly esp thr val glu val gly ala arg arg leu
 481/161 511/171
 cgg gtc gtt ggc att ggc cgg acc met tcc acc ggc cgg gcc wgt atc ccc aat gtc ttc ccc
 cgg val val gly ile val pro asn ser thr ala lle ala lys lle phe asn val phe leu
 541/181 571/191
 acg acc ggg ggc tta cgg aca ttc ggg tac act ggg cgg ccc aat atc acc tcc atc ggg
 thr thr gly leu gln lys leu ala tyc ser gly gln pro asn ilr thr ser lle gly
 601/201 631/211
 atc ata ggt atg ccc cga tag cgg cgg ggg atg tac gag acc ttc gat cgg ggg gca gtc
 ile lle gly met pro arg gln leu pro gly tyc gln thr phe esp arg val gly ala
 661/221 691/231
 gtc aat gac ttc gtc cgg cca ttg aag gtc gca cgg aat tcc atc tac atc gtc gat gtt
 val asp leu val arg pro leu lys val ala val can ser lle ser lle val als val
 721/241 751/251
 ttg ctt cgg att gtc ggg gtc ctt atc gtc ggc tcc gtc gta tac ctt tcc gct act gag
 leu leu trp ile val als val lle val lle gly ser val val tyr leu ser als leu glu
 781/261 811/271
 cgg ctc cgt gac ttc ggg gtc ttc aag ggg att gtc acc cca acc ccc tcc atc gtc act aig gca
 arg leu arg esp phe ala val phe lys ala lle gly thr pro thr arg ser ile met als
 841/281 871/291
 ggg ctc gca tta cag gca ctt gtc gat gtc ttc gat ggg gtc gtc gtc gtc
 gly lle als ala leu gln als lle val lle als lle lle als als val val gly val val leu
 901/301 931/311
 gng cgg gtc ttc gca cca ctt gtc atg acc gtc gtc gtc gtc gtc gtc gtc gtc
 als gln val leu ala pro leu phe pro met lle val als val pro val gly ala tyr leu
 961/321 991/331
 gcg cta ccc gca gtc gng ato gca acc ggt ctc ttc gct met met gtt gca ggg ttg aac ccc
 als leu pro val als als lle val lle gly leu phe als ser val als gly leu lys arg
 1021/341 1051/351
 gtc gtc acc gtc gac acc gca cgg ggg ttc gga ggt acc tag
 val val thr val esp pro als gln als phe gly gly pro AMB

SEQ ID N° 8H

29/185

31/11

CCA GGC CGA GCG AAC CGT CGA TTC CAT GGG TGT CGA CGC ATT CTC GGT CAA GGC CGG CGC
 arg gly arg ala asn arg arg phe his gly cys arg arg ile asn gly gla gly arg arg
 61/21 91/31
 GGC AGG ACC GTT CCT CGG TTC GAC ACC ATT CGC CCA AAT CGA CCT GCC CCA GGT TCC TCG
 gly arg thr val pro gly phe asp thr ile arg pro asn arg pro ala pro gly cys ser
 121/41 151/51
 TGC GGC TCG CGT CTT GGC TGC CGC CCC ACT AGC GAC TCG GCG GTC GAC GAT CGG GCA GGC
 cys ala trp arg leu gly cys arg pro thr ser asp cys ala val asp asp pro ala gly
 181/61 211/71
 CAC GTC ACC CGG AAA CGT CGC CGT CGG GGC ACC AGA GCA CGG ACC CGG CAT CGG CGG
 his val ser ala lys arg ala arg val arg gly thr arg ala arg thr arg his ala ala
 241/81 271/81
 GGT CTC CGA CGG TCG GGC CGC ATC GAC GGC GGA CGA CGT CGG GGT GTC GAG CAC GCT GGG
 gly leu gly arg ser gly ala ile asp ala gly arg gly arg gly val gln his ala gly
 301/101
 CGG AAC CCT CGG CGA CGA TC
 pro lys phe arg arg arg

SEQ ID N° 9A

FIGURE 9A

32/11

GAG GCG CGC CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC CTG GTC AAG GCG GGC GCG
 glu ala glu arg thr val asp ser met gly val asp ala phe val val lys ala gly ala
 62/21 92/31
 CGA GGA CGG TTC CTG GGT TCG ACA CGA TTC CGC CAA ATC GAC CTG CGG GAG GGT GCT GGT CGT
 ala ala gly pro phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala arg
 122/41 152/51
 GCG CCT CGC CTG TTG GCT CGC CGC CCA CTA CGG ACT CGG CGG TCG ACG ATC CGG GAG GGC
 ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly
 182/61 212/71
 ACG TCA CGG CGA AAC GTC ACC CGC TTC CGG CGA CGA GAC CGC CGA CGC ATC CGG CGG
 thr ser ala arg asn val thr ala phe gly ala pro glu his gly pro gly met pro arg
 242/81 272/91
 GTC TCG GAC GGT CGG CGC CGA TCG ACG CGG GAC GAG GTC CGG CGG TCG ACG ATC CGG CGG
 val ser asp gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu gly
 302/101
 CGA AAC CTC CGC GAC GAT C
 arg asn leu gly asp asp

SEQ ID N° 9B

FIGURE 9B

30/185

33/11

AGG CCG AGC GAA CGG TCG ATT CCA TGG CTG TCG AGC CAT TCG TGG TCA AGG CCG CGG CGG
 arg pro ser glu pro ser ile phe trp val ser thr his ser trp ser arg pro ala arg
 63/21 93/31

CAG GAC CGT TCC TGG GTT CGA CAC CAT TCG CCC AAA TCG AGC TGC CGC AGG TTG CTC GTO
 gln asp arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val
 123/41 153/51

CCC CTC GCG TCT TGG CTG CGG CCC CAC TAG CGA CTC CGC CGT CGA CGA TCC GGC AGG GCA
 arg leu ala ser trp leu pro pro his AMB arg leu arg arg arg ser gly arg ala
 183/61 213/71

CGT CAG CGG GAA AGC TCA CGG CGT TCG GGG CAC CAG AGC AGC GAC CGG GCA TGC CGC GGC
 arg gln arg glu thr ser pro arg ser gly his gln ser thr asp pro ala cys arg gly
 243/81 273/91

TCT CGG ACG CTC GGG CGG CAT CGA CGC CGG AGG AGG TGG CGG TGT CGA GCA CGC TCG GGC
 ser arg thr val gly arg his arg arg arg thr arg ser arg cys arg ala arg trp ala
 303/101

GAA ACC TCG GCG AGC ATC
 glu thr ser ala thr ile

SEQ ID N° 9C

FIGURE 9C

31/11

TTA ACG ACT CAG AGC GAA ACG CTT GAA CGG CGA GGT CGC TCC GGA CAC GAA TTT GAC TCG
 leu thr thr gln thr gln leu glu pro arg gly arg ser gln his gln phe asp ser
 61/21 91/31

GCT CTC TGG CAA TTG AAG GTG AGC TGC GAG CAG CGG CGT GAC CGC AGC ATC GTT GGC CTT CGC
 ala leu trp gln leu lys val ser cys glu gln phe gly asp arg ile val gly leu ala
 123/41 151/51

ATC AAT CGC CGG CTC CGC GAC GTA GAT ATT CAG CTC AGC CGT CGK ACC GAC CTC GAC CAG
 ile asn arg arg leu ala asp val asp asn gln leu thr val gly thr asp leu asp gln
 181/61 211/71

GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTG CGT CAT CGC CTA AGG
 gly ser phe val thr ala gln leu asp ala asp asp his arg val gly his arg leu arg
 241/81 271/91

CTA CCG TTC TGA CCT GGG GCT GGG TGG CGG CGG AGC ACG TGA GGC AGC TCA TGT CTC AGC
 leu pro phe CTA pro gly ala ala trp ala phe pro thr CTA gly thr ser cys leu ser
 301/101 331/111

GGC CCA CGG CCA CCT CGG TCG CGA GCA GTA TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC
 gly pro pro pro pro arg ser pro ala val Cys gln his val gln met thr pro arg ser
 361/121 391/131

CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG AGC AGC TTG CGG CTC GTG AGC GCA CGC CGC
 leu val arg ile val gly val val ala thr thr leu ala leu val ser ala pro ala
 421/161

GCG GGT CGT GCG GCG CAT CGG GAT C

gly gly arg ala ala his ala asp

SEQ ID N° 10A

FIGURE 10A

31/185

32/11

TAA CGA CTC AGA CGG AAA CGC TTG AAC CGC GAG GTC GGT CGG GAC ACC AAT TTG ACT EGG
 OCH arg leu arg arg lys arg leu asn arg glu val ala pro asp thr asn leu thr arg
 62/21 92/31

CTC TTT GGC AAT TGA AGG TGA CCT CGC AGC AGG CGG GTC ACC GCA TCG TTG GGC TTG CCA
 leu phe gly asn OPA arg OPA ala ala ser ser arg val thr ala ser leu ala leu pro
 122/41 152/51

TCA ATC GGC GGC TCG CGG AGG TAG ATA ATC AGC TCA CGG TGG GGA CGG ACC TCG ACC AGG
 ser ile ala gly ser arg thr AMB ile ala ser ser pro leu gly pro thr ser thr arg
 182/61 212/71

GGT CCT TTG TGA CTG CGG GGC TTG ACG CGG AGG ACA GAG TCG GTC ATC GGC TAA GGC
 gly pro leu OPA leu pro gly leu thr arg thr the thr glu ser val ile ala OCH gly
 242/81 272/91

TAC CGT TCT GAC CTG CGG CTC CCT CGG CGC CGA CGA CGT GAG GCA CGT CAT GTC TCA CGG
 tyt arg ser asp leu gly leu arg gly arg arg arg glu ala arg his val ser ala
 302/101 332/111

GCC CAC CGC GAC CTC CCT CGG CGG CAG TAT GTC AGC ATG TGC AGA TGA CTC CAC CGA CGG
 ala His arg his leu gly arg arg gln tyr val ser met cys arg OPA leu his ala ala
 362/121 392/131

TTG TTC GCA TCG TTG GTC TGG TTG TTG GCA CGA CCT TGG CGC TTG TGA CGG CGC CGG CGC
 leu phe ala ser leu val ser trp leu arg arg pro trp arg trp OPA ala His pro pro
 422/141

CGG GTC GTC CGG CGG ATG CGG ATC
 ala val val phe arg met arg Ile

SEQ ID N° 10B

FIGURE 10B

33/11

AAC GAC TCA GAC GGA AAC GCT TGA ATC CGG AGG TCG CTC CGG AGA CGA ATT TGA CTC CGG
 asn asp ser asp gly asn ala OPA thr ala arg ser leu arg thr pro ile OPA leu gly
 63/21 93/31

TCT TTG GCA ATY GAA GGT GAG CTG CGA CGA CGC CGG TGA CGG CAT CGT TGG CCT TGC CAT
 ser leu ala ile glu gly glu leu arg ala ala gly OPA pro his arg trp pro cys his
 123/41 153/51

CRA TCG CGG CCT CGC GGA CGT AGA TAA TCA GCT GAC CGC CGT TGG GAC CGA CCT CGA CGA CGG
 gln ser pro ala arg gly arg arg OCH ser ala His arg trp asp arg pro arg phe gly
 183/61 213/71

CTC CCT TGT GAC TGC CGG CCT TGA CGG GGA CGA CGA CGC AGT CGG TCA TGG CCT CCT AAG GCT
 val leu cys asp cys arg ala OPA Arg gly arg pro gln ser arg ser ser phe lys ala
 243/81 273/91

ACC GTT CTG ACC TGG GGC TGC GTG CGC CGC CGC GAC GAC GTC ATG TCT CAG CGG
 thr val leu the trp gly cys val gly ala asp asp val arg His val met met gln arg
 303/101 333/111

CCC ACC CGC ACC TCG GTC CGC CGC AGT ATG TCA CGA TGT CGA GAT CGG TCC AGG CGG CCT
 pro the ala Thr ser val ala gly ser met ser ala His asp ala asp asp for the gln pro
 363/121 393/131

TGT TCG CAT CGT TGG TGT CGT GGT TGC CGA CGC CCT GGC GCT GGT CGG CGC ACC CGC CGG
 cys ser his Arg trp cys Arg gly cys asp asp leu gly ala gly glu arg Thr arg arg
 423/141

CGG TCG TGC TGT CGA TGG CGG TC
 arg ser cys Arg ala cys gly

SEQ ID N° 10C

FIGURE 10C
FEUILLE DE REMPLACEMENT (REGLE 26)

32/185

31/11
 CCC GAA GAG GTC CGC GGT TTT ATT TAA AAA KIT TGT GTC AGA AAC CGG GGT ACC
 pro glu glu val pro arg phe val asp phe OCH lys tie cys val thr lys arg gly thi
 61/21 91/31
 AAC GCA TAA AAC CTA GTC CCT GGG CGC GAT TCA AGG AAC GAG TGG GGG TAG TCA
 lys als OCH asn Ieu val pro gly als als asp ser thr lys thr glu trp gly RME see
 121/42 151/51
 GGG CGG TGC ATT CGG AGG ACC CTC TAG GAG CGG CTG GTC GCA RCG CGG ATG AGT CGG CGG
 gly als cys ile pro thr thr leu tyr asp pro leu val als thr pro met ser als pro
 211/61 211/71
 AGG AAG GCG GAG CGA CGG OCT CGC GGC AGT GAC CGG CGA GTC CAT GGT
 the lys als glu arg arg als als gly als asp arg arg gly ser arg arg val asp gly
 241/81 271/91
 CAG CRC CGG CAC CGG ACC GGT AGG GAT CGC GGC TGC GGT TAC CTC CCT CGG CGT CAA CGC
 his his arg pro his pro thr gly the asp arg als ser gly tyr arg arg arg gln arg
 301/101 331/111
 GCT GGA CAG CAT CGG TCC CGG CTC GGT CAA TCA ACT CAT CGC CGG CGN CAA CGA AGT
 ala gly gln als arg ser pro leu gly gln cys the his als als pro glu arg thr als
 361/121 391/131
 CAA CGC TTG AAC CGG GNC CGG CGG GGC TCC CAA CCT GTC GGC CGC CGT CGA CGT AGT
 gln pro leu ser arg val pro als cys arg pro ser als als gly val phe leu arg asp
 421/141 451/151
 AGA CGC AGG CGC ATG GAA ATC CTG GGC AGC CGG ATG CTC CCT CGG CGG GAC TAT CGG
 arg thr arg als met glu ile leu als ser arg met leu leu arg pro als asp tyr gln
 481/161
 CGG TCG CTG AGC TTC TAC CGT GAC CGG ATC
 arg ser leu ser phe tyr arg asp gln ile

SEQ ID N° 11A

FIGURE 11A

32/11
 CGG ARG AGG TOC CGG CCT TTC TTA ATT TTT ATT AAA AAA TTY GYG TCA CAA ACC CGG GCA CGA
 pro lys arg ser phe val leu leu ile phe lys lys phe val ser gln ser gly val phe
 62/21 92/31
 AGG CAT AAA ACC TAG TAC CTC TGG CGG CGG ATT CAA CGA AAA CGG AGT CGG GCT AGT AAC CGA
 arg his lys thr ARK tyr leu gly arg arg ile gln arg lys pro ser gly gly ser gln
 122/41 152/51
 GGG CGT GCA TTC CGA CGA CGC CCT TGT AGC ACC CGG TGG CGA CGC CGA TGA GTC CGG CGA
 gly arg als phe arg arg phe cys the thr arg trp trp gln arg arg CGA val arg arg
 182/61 212/71
 CGA AGG CGG AGC CGC CGG CTC CGG CGG CCT CCT CGG GAA CGC CGC CGC TGG ARG GTC
 arg arg pro ser als gly phe pro als leu the als als gln als als gln trp met val
 242/81 272/91
 ACC AGC CGC ACC CGA CGG GTC CGA CGG ATC CGG CCT CGG CGG GTC AGC CGC GTC AGT CGG
 the thr als arg thr arg pro val arg ile als pro arg val thr val als val esn als
 302/101 332/111
 CTC GRC AGC ATC GGG CGG CGC CGC TGG GTC ATT GCA CCT ATT CGG CGC CGG AAC GAA CGG CTC
 leu asp ser ile gly phe arg trp val esn als leu met gln arg arg esn glu gln ieu
 362/121 392/131
 ARG CCT TCA AGG GGG TCC CGG CCT GGC GTC CGG CGG CGG CGG CGG TGC CGG TAC GTC ATT
 asn pro GPR the gly ser arg pro ala phe arg phe arg pro pro als cys arg tyr val ile
 422/141 452/151
 GAG AGA CGG CGA TGA AAA TCC TGG CGA CGG CGA TCC TGC TTC GCT CGG CGG AGT AAC AGC
 arg thr gly pro trp lys ser trp pro als gly cys tyr phe gly arg arg thr ile asy
 482/161
 GUY CGC TGA GGT TCT AGC GTC AGC AGA TC
 gly arg GPR als ser thr val thr arg

SEQ ID N° 11B

FIGURE 11B
FEUILLE DE REMPLACEMENT (REGLE 26)

33/185

33/11

CGA AGA GGT CCC CGG TTT TGT TAA TTT TTA AAA ATG TTC TGT CAC AAA GGG GGG TAC CAA
arg arg gly pro pro phe cys OCH phe leu lys asn leu cys his lys ala gly tyr glu
63/21 93/31

GCC ATA AAA CCT AGT ACC TGG GGC CGG GGA TTC AAC GAA AAC CGA GTG GGC GTC GTC AGG
gly ile lys pro ser thr trp gly gly gly phe asn glu asn arg val gly val val arg
123/41 153/51

GCC GTG CAT TCC GAC GAC CCT GTC CGA CCC GCT GCT GGT AAC GGC GAT GAG TGC GGC GAC
gly val his ser asp asp pro val arg pro ala gly gly asn ala asp glu cys ala asp
183/61 213/71

GAA GGC CGA CGG AGG GGC TGC CGG CGC TGA CGG CGC CGG AAG CCG CCG AGT GGA TGG TCA
glu gly arg ala thr gly cys arg arg OPA pro pro arg lys pro pro ser gly trp ser
243/61 273/91

CCA CGG CCC GCA CGT GAC CGG TAC GGA TCG CGG CTC CGG TTA CGG TCG CGG TCA ACC CGC
pro pro pro ala pro asp arg tyr gly ser arg leu gly leu pro ser pro ser thr arg
383/101 383/111

TGG AEA GCA TCG GTC CCC GCT GGG TCA ATG CAC TCA TCC AGC GGC GCA ACG AAC AGC TCA
trp thr ala ser val pro ala gly ser met his ser cys ser ala ala thr asn ser ser
383/121 383/131

AAC CTT GAA CGG GGT CCC CGG CTG CGG AGC CTC GGC CGG CGT GGC GCT AGG TGA TAG
thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg ala ala thr OPA AMB
423/141 483/151

ACA CAG GGC CAT GGA AAT CCT GGC CAG CGG GAT GGT ACT TCG GGC GGC GGA CTA TCA GGC
thr glu gly his gly asn pro gly glu pro asp ala thr ser ala gly gly leu ser ala
483/161

GTC GCT CTT CTA CGG TGA CCA GAT C
val ala glu leu leu pro OPA pro asp

SEQ ID N° 11C

FIGURE 11C

partie de la séquence nucléotidique de RgII

1/1 31/71

CST CGC CST CAA CSC GCT GGA CAG CAT CGG TCC CGG CTG GGT TAA TGG ACT CAT GCA CGG
arg arg arg glu arg ala gly glu his arg ser pro leu gly glu cys thr his ala ala
61/21 91/31

CGG QAA CGA ACA GCT CAA CCC TTG AAC CGG GTC CGG CGC TGC CGA CGC CGC CGG CGC CGC CGC
pro glu arg thr ala glu pro leu asn arg val pro ala cys arg pro ser ala ala gly
121/41 151/51

CTG CGG CTA CGT GAT AGA CAC AGG GGC ATG GAA ATC CTC CGG AGC CGG ATG CTA CTT CGG
val pro leu arg asp arg his arg ala met glu ile leu ala ser arg met leu leu arg
181/61 211/71

CGG CGG SAC TAT CAG CGG TCG CTG AGC TTC TAC COT SAC CAG AGC
pro ala asp tyr glu arg ser leu ser phe tyr arg asp glu ile

SEQ ID N° 11A'

FIGURE 11A'

34/185

1/1 31/11
 GTC GGC GTC AAC GCG CTG GAC AAC ATP CTT GGT CCC CGC TGG GTC ATG GCA CTC ATG CAG CGC
 val ala val asp ala leu asp ser ile gly pro arg trp val ala leu met gln arg
 51/21 91/31
 CGG GAA CGG CTC AAC CCT TGA ACC GGG TCC CGG CCT GCC GAC CCT CGG CGG CGG CGG
 arg asn glu leu ser pro GFA thr gly ser arg pro ala asp pro arg pro pro ala
 121/41 181/51
 TGC GCG TAC GTG ATA GAC ACA CGG CGA TGG AAA TCC TGG CGA CGA TGC TAC TTC CGC
 cys arg tyr val ile asp the gly pro trp lys ser trp pro ala gly cys tyr phe gly
 181/61 211/71
 CGG CTC ACT ATC AGG GUT CGC TGA GCT TCT ACC GTG ACC AGA TC
 arg arg thr ile ser gly arg GFA ala ser thr val thr arg

SEQ ID N° 11B'

FIGURE 11B'

1/1 31/11
 TCG CCG TCA ACG CGC TGG ACA GCA TCG TCC GTC CGG GTC ATG GAG TCA TGG AGC CGC
 ser pro ser thr arg trp thr ala ser val pro ala gly ser met his ser cys ser ala
 51/21 91/31
 GCA ACG AAC AGC TCA AAC TTT GAA CGG GAT CGC CGC CTC CGG AGC CTC CGC CGC CGC CGC
 ala thr asn ser ser thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg
 121/41 181/51
 CGC GCT ACG TGA TAG ACA CAG GGC CAT GAA ATG CCT CGG CGG CGG GAT GCT ACT TCG CGC
 ala ala the GFA AMG thr gln gly his gly asp pro gly gln pro asp ala thr ser ala
 181/61 211/71
 GGG GGA CTA TCA CGG GTC CCT GAG CTT CTA CGG TGA CGA GAT C
 gly gly leu ser ala val ala gln leu leu phe GFA pro asp

SEQ ID N° 11C'

FIGURE 11C'

séquence Pv0546c prédictée par par Cole et al. (Nature 333:537-541) et contenante SeqIDN°

1/1 31/11
 atg gas atc ctg gcc agc cgg atg cta ctt cgg ccc ggg gag taa gag cgg tgg atg agc
 Met glu ile leu ala ser arg met leu leu arg pro ala asp tyr gln arg ser leu ser
 61/21 91/31
 ttc tac cgt gag atc ggg ctg ggc att gca cgt gas tac ggg gcc ggc aca gtg ttt
 phe tyr arg asp gln ile gly leu ala ala ala arg gly tyr gly ala gly thr val phe
 121/41 181/51
 ttc gcc cgt daq tca ctc gag ctc gag ggc tcc ggc gag ccc gag cat tcc cgg gga
 phe ala gly gln ser leu leu gln leu ala gly tyr gly gln pro asp his ser arg gly
 181/61 211/71
 cer trt acc ggc ggg cgg tgg atg cgg cgg cgg cgg gag cat tcc gag gag
 pro phe pro gly ala leu phe leu gln val arg arg leu gln ala thr gln thr gln leu
 241/81 271/81
 gtc aac tca ggc gtc tgg tgg amc get cgc gag ccc cgg cgc gca cgg tgg ggc tgg tgg
 val ser arg gly val ser ile ala arg gln pro arg arg gln pro trp gly leu his gln
 301/101 331/111
 arg cat gtc acc gca gag ggg atc atm ctc ata ttc utc gag gtt ccc gag ggt cac
 met his val thr asp pro asp gly ile thr leu ala phe val gln val pro glu gly his
 361/121
 ccc ctg cgt aca gag acc wgt ggc tgg
 pro leu arg thr asp thr arg ala GFA

SEQ ID N° 11D

FEUILLE DE REMPLACEMENT (RÈGLE 26)

25 / 30

ORGANISATION OF THE POLICE FORCE IN THE STATE OF KARNAKATA

1/1 31/11
 tag tcc ggg cgt gca ttc gag gag got gta cta ccc gct ggt ggc gag tac gag gat gat tgc
 AMB ser gly arg ala phe asp asp ala val leu pro ala gly gly asn ser asp asp cys
 61/21 91/31
 gcc gag gaa ggc ctc cga cgg gct gac ggc gat gag cgc cgc gga aac cgc cga gtc gag
 ala asp glu gly leu arg arg ala ala gly sia asp arg gly ser arg ser val asp
 121/41 151/51
 ggt cac cgc cgc cgg cac ccc ggt gag gat cgc gac tag ggt tgc cgt cgc cgt cca
 gly his arg arg pro his pro thr gly ala asp arg als ser gly cys arg arg arg gln
 181/61 211/71
 cgc gct gga cag cat cgg tcc ccc ctg ggt taa tgc act cat gca gcg ccc cas cgs aca
 arg ala gly gin his arg ser pro leu arg gln cys thr his ala ala pro gln arg thr
 241/81 271/91
 gct cca ccc ttg aac cgg gtc ccc gca tgc cgg ccc tag gca gca ggc ggt ccc cta cgt
 ala gin pro leu asn arg val pro ala cys arg pro ser ala ala gly val val pro leu arg
 301/101 331/111
 gat aca cac egg gtc arg gaa atc ctg gcc aca cgg ctg cta ott ccc ccc gca gag bat
 asp arg his arg als met glu ile leu ala ser arg met leu leu arg phe als asp tyr
 361/121 391/131
 csg cgg tag ctg ayc ttc bac cgt gag cag atc ggg ctg gca atc gco cgt gca tac ggg
 gln arg set leu ser phe tyr arg asp gln ala gly leu ala ile ala arg glu tyr gly
 421/141 451/151
 gcc Ggc aca gtc ttg ttc tcc gca ggt gag tca ctg ctc gca ctg gcc ggt tac ggc gag ccc
 ala gly thr val phe phe ala gly gln ser leu leu glu leu als gly tyr gly glu pro
 541/161 551/171
 gag cat tcc cgg gga cct ttt ccc ggc gcy atg tgg ccc gag gtg ccc gag ccc ott gag gct
 asp his ser arg gly pro phe pro gly ala leu pte leu gln val arg asp leu glu ala
 561/181 571/191
 acc cag acc gag ctg gtc ayc cga gca gtc atc gtt ccc gag ccc gag ccc gag ccc gag gaa ccc
 thr gln thr glu leu val ser arg gly val ser ilv ala arg glu pro arg arg glu pro
 601/201 631/211
 tgg ggc org cac gag atg cat gtg acc gac cca gac ggg atc sma ctg ata ttc gtc gag
 trp gly leu his glu met his val thr asp pro phe gly lie thr leu lie phe val glu
 661/221 691/231
 gat ccc gag ggt cac ccc crg cgt aca gag acc egg ggc tga
 val pro glu gly his leu leu arg the asp thr his ala DPA

SEC ID N^o 114

FIGURE 11.8

36/185

1/1 31/11
 gac cga egg gat ttc ggc act aac tcc gec tgt aag gca acg cca ggt ctt cat gtc gag
 asp arg arg asp phe ala thr asn ser ala cys lys ala thr arg gly leu his ala glu
 61/21 91/31
 gac gta gac egg aag aga cag gga aac tca tga cgt ccc gta ccc gac cgg cat tot gtc
 asp val asp arg lys arg gln gly ser CTA CTA arg arg val pro asp arg his ser val
 121/41 151/51
 gaa tct ttc cgg gtt cag cca cca tcc aca cag aag cgg gga cca gac cgg gag gac gac
 glu ser phe arg val gln gln gln ser thr gln lyc arg gly pro asp arg glu asp asp
 181/61 211/71
 gcg gcc cgg gcc gct tcc egg cga ctc tcc gag taa gac ccc aat ccc ggg tcc gtc tgt
 ala ala arg ala ala ser gly arg val ser glu CTC asp gln ser his gly ser val cys
 241/81 271/91
 gac aac cgg ggg gaa ttc sat cgg aat gac ggg ggg acc gca trg ccc cgg tcc ccc agg
 asp asn arg ala glu phe asn arg met ala gly gln thr gly leu arg arg ser pro arg
 301/101
 aac ccc cgg aat gat c
 aac leu arg ser asp

SEQ ID N° 12A

FIGURE 12A

1/1 31/11
 acc gaa ggg att tcc cga cta act cgg ccc gta aag cca aac ccc gag gtc ttc atc ccc agg
 thr glu gly ile ser arg leu thr arg pro val arg gln aag glu val phe met pro arg
 61/21 91/31
 acg tcc aca gga aca gac egg gaa gat gat gac ccc ggg tcc ccc aac gca att ccc tcc
 thr AMB thr gly arg asp aac glu ala asp asp val ala tyc arg thr ala ala leu ser
 121/41 151/51
 agt ctt tcc gag ttc agg aac aat cgg ccc aca aca aac ggg gag ccc ggg aag egg arg aac
 ser leu ser glu phe ser asn aac arg his arg ser gly asp gln thr gly arg thr thr
 181/61 211/71
 cgg ccc ggg ccc ctt cgg gcc gag tgt ccc aat aag acc aca gtc aac ggt ccc ccc tgt gaa
 arg pro gly pro leu arg ala gln cys leu ser lys thr arg val thr gly pro cys val
 241/81 271/91
 aca acc gcm cgg aat tcc att ggg tgg ccc ggg gya ccc gat tcc gca ggt ccc cya gga
 thr thr ala arg arg asn ser ile gly trp arg ala gly pro asp cys ala gly his arg gly
 301/101
 acc tcc gpa gty aac
 thr ser gly val ile

SEQ ID N° 12B

FIGURE 12B

37/185

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1/1          31/11
cog aag gaa ttt cyc gac taa ctc ggc ctg taa ggc aac tqg agg act cca tyc oga gga
pro lys gly phe arg asp GCH leu gly leu OCH gly amn als arg ser ser cys arg gly
61/21         91/31

cgt ags cag gaa gag acs ggg aag ctg atg acg tgg cgt acc gta cgg cca ttc tgg cpa
arg arg gln glu glu thr gly lys leu met the ser arg thr gly pro pro phe cys arg
121/41        151/51

gtc ttt cog agt tca gca aca atc gac aca gaa ggg acc aca aga ggg gaa gca cgc
val phe pro ser ser ala ala thr ile asp the ala glu gly thr the arg pro gly gly arg arg
181/51        211/71

ggc cog ggc wcc ttc ggg acc act gtc tga gta agg cca qag tca cgg gtc cgt gtg tga
gly pro gly arg phe gly pro ser val CTA val big pro glu ser arg val val arg val glu
241/71        271/91

caa cog cgc gga att cas tcc gat ggc ggg cgg cgc agg acc tqg cgg ccc acc gaa gaa
glu pro arg sly ille gln ser asp sly gly arg esp ser sly ille sly pro val thr glu glu
301/101

ctt cog gag tga tc
pro trp cts CTA

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SEQ ID N° 122

FIGURE 12C

1/1
GGG ANT TCG TTG CGC GAT CGA TTG TTT GTC CGG TTT GCG AAA AAC ACT TGA AGT CCT TTA
gly ile ser leu pro asp gly leu phe val arg phe gly lys asn the CTA ser pro phe
61/21
TAT TGC CAN TGC TGG AAA TGG ACA TTC CAA TAT TGC CGG ATT TAA CGG AAC AGG GTG AGG
try trp gln cys trp lys try cys gln try cys ala ser DCH pro asn thr val arg
121/41
GGG GGG CCA CGG TTT GTC CGG GGG CCA GCA ATG CGG CGG CGG TGG ACC GAA CGC ADC
gly gly gln als phe val pro gly pro als ser als ser asp arg leu thr gln als ser
181/61
ATT TTG TTG TGT CGG CGG CTT CCTT CTC GAT CGG CGG CGG CGG TCT GCT CGA CGG CGG CCT CCT
met leu leu cys gln ala gly leu gln ala ser val pro als leu als gln pro als ser
241/81
TCA AAA CAG GGT GAA CCT AAC GAG TCA RKA AGG GAA AGG UCT GAA CGG CGG CGG CGG CGC TCC
ser lys gln val gln leu asn asp ser arg the gln the leu gln pro arg arg arg ser
301/101
CGA CGC CAA TTT GAC TCG CCT CCT TGG CAA TTG AAC GTC AGC TGC GAG GAG CGG CGG CGT GAG
gly his gln phe asp ser als leu trp gln als lys val ser cys glu gln pro gly asp
361/121
CGC ATC GTT CGC CTT CGC ATC AAT CGC CGG CTC CGC GAC GTC GAT ANT CGG CTC ACC AGT
arg ile val gly leu als xle asn arg arg lys als asp val asp asp gln leu the val
421/141
CGG ACC GAC CTC GAC CAG GGG TCG TTT GTC AGT CGT CGG CTT GAC GCG CGC GAC CGC AGA
thr arg thr asp his gln gln gln phe val the ala gln leu asp als asp asp his arg
481/161
CTG GGT CAT TGC UTR AGG CTA CGG TGC TGC TGA CCT CGG GGT CGG CGG CGG CGG CGG CGG CGA
val gly his arg leu arg leu pro phe CTA pro gly als als als phe the CTA CGA
541/181
CGG ACC TCA TGT CTC AGC CGC CCA CGG CGG CGA GCA GTC TGT CAG CAT CTG
gly thr ser cys leu ser gln phe pro pro pro pro arg ser pro als val cys gln his val
601/201
CGG ATG ACT CGA CGC AGC CCT GTG CGC ATC GTT CGT CGG GTC CGT CGG CGG CGC AGG ACC TTG CGG
glu met the pro arg ser leu val arg ile val gln val val val als thr the leu als
661/221
CTG CTC AGG CGA CGC CGG CGC CGG CGT CGG CGC GCA GTC CGG CGC GCA GTC CGT CGC GAT C
ile val ser val als gln gln asp als als als als als asp
721/241

卷之三

FIGURE 125

FEUILLE DE REMPLACEMENT (RÈGLE 26)

38/185

32/11

GGA TTT CGT TGC CGG ATG GAT TGT TTG TAC GGT TTG GGA AAA ACA CCT GAA GTC CCT TTT
 gly phe arg cys phe met asp cys leu tyr gly leu gly lys thr leu glu val leu phe
 62/21 52/31

ATT GGG AAT GCT GGA AAT GGA CAT TCC ATT GCG CGA ATT AAC CGA ACA CGG TGA CGG
 ile gly ass ala gly asn gly his ser asn ile ala arg ile asn arg thr arg OPA gly
 122/41 152/51

GGG AAG CGT TTG TAC CGG GGC CAG CAA GCG CGG ACC GGT TGA CGG AAG CCA GCA
 gly gly lys arg leu tyr arg gly gln gln ala pro pro thr gly OPA pro lys pro ala
 182/61 212/71

TGT TGT TGT GTC AGC CGG GGC TTG CTC TCG ATG TCC CGG CCT TGG CTG GAC CGG CCT CTT
 cys cys cys val ser ala gly leu val ser met ser arg pro trp leu asp pro leu leu
 242/81 272/91

CAA AAC AGG TTG AAC TTA ACG ACT CAA GAA CGG AAA CGG TTG AAC CGG GAC GTC CCT CGG
 gln ass arg leu asn leu thr the gln gln arg lys arg leu asn arg asp val ala pro
 302/101 332/111

GAC ACC AAT TTG ACT CGG CTC TTT CGC AAT TGA AGC TGA GCT CGG AGC AGC CGG GTG ACC
 asp thr ass leu thr arg leu phe gly ass OPA arg OPA ala ala ser ser arg val thr
 362/121 392/131

GCA TCG TTG CGC TTG CCA TCA ATC CGC CGC CGC TCG CGG AGC TAG ATA ATC AGC TCA CGG TTG
 ala ser leu ala leu pro ser ile ala gly ser arg thr AMB ile ile ser ser pro ile
 422/141 452/151

GGA CCC ACC TCG ACC AGC CGT CCT TTG TGA CTC CGG CGC TTG ACC CGG AGC ACC ACA GAG
 gly pro thr ser thr arg gly pro leu OPA leu pro gly leu thr arg the thr thr glu
 482/161 512/171

TGG GTC ATC GCG TAA GGC TAC CGT TCT GAC CTC CGG CGT CGG CGC CGA CGA CGT GAG
 ser val ile ala CGH gly tyr arg ser asp leu gly leu arg gly arg arg arg glu
 542/181 572/191

GCA CGT CAT GTC TCA CGC CGC CGC CGC CGC CGC CGA TAT GTC AGC ATG TGC
 ala arg his val ser ala ala his arg his leu gly arg arg gln tyr val ser met cys
 602/201 632/211

AGA TGA CTC CGC GCA GCC TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT CCT TGG CGC
 arg OPA leu his ala ala leu phe ala ser leu val sex trp leu arg arg pro trp arg
 662/221 692/231

TGG TGA CGG CGC CGC CGG CGC GTC GTG CGC CGC ATG CGG ATC
 trp OPA ala His pro pro ala val val pro arg mett arg ile

SEQ ID N° 13B

FIGURE 13B

39/185

33/11

GAT TTC GTT GCC CGA TCG ATT GTT TGT AGG GTT TGG GAA AAA CAC TTG AAG TCC TTT TTA
 asp phe val ala arg trp ile val cys thr val trp glu lys his leu lys ser phe leu
 63/21 93/31

TTC GCA ATG CTC GAA ATG GAC ATT CCA ATA TTG CGC GAA TTA ACC GAA CAC GGT GAG GGG
 leu ala met leu glu met asp ile pro ile leu arg glu leu thr glu his gly glu gly
 123/41 153/51

GGG GCA AGC GTT TGT ACC GGG GCC AGC AAG CGC CGC CGA CGG GTT GAC CGA AGC CGG CAT
 gly ala ser val cys thr gly ala ser lys arg arg arg pro val asp arg ser gln his
 183/61 213/71

GTT GTT GTG TCA GCG CGG GCT TGG TCT CGA TGT CCC GGG CTT CGC TGG ACC CGC TTC TTC
 val val val ser ala arg ala trp ser arg cys pro gly leu gly trp thr arg phe phe
 243/81 273/91

AAA ACA GGT TGA ACT TAA CGA CTC AAC GGA AAC GCT TGA ACC GCG ACC TCG CTC CGG
 lys thr gly GFA thr GCH arg leu lys sas gly asp ala GFA thr ala thr ser leu arg
 333/101 333/111

ACA CCA ATT TGA CTC GGC TCT TTG GCA ATT GAA GGT GAG CGT CGA GCA GCG GGG TGA CGG
 thr pro ile GFA leu gly ser leu ala ile glu gly glu leu arg ala ala gly GFA pro
 363/121 383/131

CAT CGT TGG CCT TGC CAT GAA TCG CGG GCT CGC GGA CGT AGA TAA TCA GCT AAC CGT TGG
 his arg trp pro cys his gln ser pro ala arg gly arg arg GCH ser ala his arg trp
 423/141 453/151

GAC CGA CCT CGA CGA GGG GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT
 asp arg pro arg phe gly val leu cys asp cys arg ala GFA sas gly arg pro gln ser
 483/161 513/171

CGG TCA TCG CCT AAG GCT ACC ATT CTC ACC TGG CGC TGG GTG GGC GCG GAC GAC GTC AGG
 arg ser ser pro lys ala thr val leu thr trp gly cys val gly ala asp asp val arg
 543/181 573/191

CAC GTC ATG TCT CAG CGG CCC ACC GCG ACC TCG GTC GCG GGC AGT ATG TCA GCA TGT GCA
 his val met ser gln arg pro thr ala thr ser val ala gly ser met ser ala cys ala
 603/201 633/211

DAT GAC TCC ACG CAG CCT TGT TCG CAT CGT TGG TGT GUT GGT TGC GAC GAC CTT GGC GCT
 asp asp ser thr gly pro cys ser his arg trp cys arg gly cys asp asp leu gly ala
 663/221 693/231

GGT GAG CGC ACC CGG CGG CGG TCG TGC CGG GCA TGC GGA TC
 gly glu arg thr arg arg arg ser cys arg ala cys gly

SEQ ID N° 13C

FIGURE 13C

40/185

partie de la séquence nucléotidique de seq13A

1/1 31/11
 GGG TCC TTT GTC ACT GGC GGG CTT GAC GCG GGC GAC AGA GTC GGT CAT GCG CTA AGG
 gly ser phe val thr ala gly leu asp ala asp his arg val gly his arg leu arg
 61/21 91/31
 CTA CGG TTC TGA CCT GGG CCT GCG TGG CGC CGG ACG AGG TGA GGC AGG TCA TGT CTC ACC
 leu pro phe GAA pro gly ala ala trp ala pro thr thr thr GFA gly thr ser cys leu ser
 121/41 151/51
 GGC CGA CGG CGA CCT CGG TCG CGG GCA GCA TGT CAG CAT GTC GAG ATG ACT CGA CGC AGC
 gly pro pro pro pro arg ser pro ala val cys gln his val gln met thr pro arg ser
 181/61 211/71
 CCT GTT CGG ATC CCT GGT GTC CGG CCT ACG ACC TGA CGG CTG GTC AGC GCA CGC GCG
 leu val arg ile val gly val val val ala thr thr leu ala leu val ser ala pro ala
 241/81
 GGC GGT CGT CGC CGG CAT CGG GAT C
 gly gly arg ala ala his ala asp

SEQ ID N° 13A'

FIGURE 13A'

1/1 31/11
 GGT CCT TTG TGA CGT CGG CGC TGG AGC CGG AGG AGC AGA GAG TGG ATC ATG CGC TAA CGC
 gly pro leu CGA leu pro gly leu thr arg the thr the gln ser val ile ala CGH gly
 61/21 91/31
 TAC GGT TCT GAC CTG GGG CTG CCT CGG CGA CGA CCT GAG GCA GGT CAT GTC TCA CGG
 tyr arg ser asp leu gly leu arg gly arg arg arg arg gln ala arg his val ser ala
 121/41 151/51
 CGC CAC CGC CAC CTC GGT CGC CGG CAG TAT GTC AGT ATG TCG AGA TGA CTC CGG GCA CGC
 ala his arg his leu gly arg arg gln tyr val ser met cys arg GFA leu his ala ala
 181/61 211/71
 TTG TTC GCA TCG TTG GTC TCG TGG TTG CGA CGA CCT TGG CGC TGG TGA CGG CGC CGC CGG
 leu phe ala ser leu val ser trp leu arg arg pro ipr arg tyr GFA ala his pro pro
 241/81
 CGG GTC CGG CGG CGC ATG CGG ATT
 ala val val pro arg met arg ille

SEQ ID N° 13B'

FIGURE 13B'

1/1 31/11
 GTC CTT TGT GAC TGG TCG CGG GGT TGA CGG CGA CGA CAA AGT CGG TCA TGG CCT AAC GCT
 val leu cys asp cys arg ala GFA arg gly arg arg pro gln ser arg ser ser pro lys ala
 61/21 91/31
 AGC GTT CTG ACC TGG CGG TGC TGG CGC CGC GAC GAG GTC AGG CGC CGC ATG TGT CAG CGG
 thr val leu the top gly cys val gly ala asp asp val arg his val met ser gln arg
 121/41 151/51
 CGG ACC CGG ACC TGG GTC CGC CGC CGG AGT AGT AGG TCA CGA TGT CGA GAT GAG TGC TGG CGG CGC
 phe thr ala thr Ser val ala gly ser met ser ala cys ala dnp asp met thr gln pro
 181/61 211/71
 TGT TCG CAT CGT TGG TGT CGT GGT TGG GAC GAG CCT CGT CGC CGT GGT GAG GAG CGC AGC CGG CGC
 cys ser his arg trp cys arg cys asp asp leu gly ala gly gln arg thr arg arg
 241/81
 CGG TCG TGC CGG CGA TGC CGA TC
 arg ser cys Arg ala cys gly

SEQ ID N° 13C'

FIGURE 13C'

FEUILLE DE REMPLACEMENT (REGLE 26)

41/185

séquence Rv1984c prédicté par Cole et al. (Nature 393:537-544) et contenant seq13A'

1/1 31/11
 atg act cca cgc aac ctt gtt tgg atc gtc gtc ggg gtc gat acg acc ttg gcg ctg
 Met thr pro arg ser leu val arg ile val gly val val val ala thr thr ileu ala leu
 61/21 91/31
 gtg aac gca ccc gac ggc egt ggt gac cat gac gat aac gtc tgg gac atc gcg gtc
 val ser ala pro ala gly gly arg ala ala his ala asp pro cys ser asp ile ala val
 121/41 151/51
 gtt ttc got cgc ggc acg cat cag gct tct qgt ctt ggc gac gtc ggt gsg gcg ttc gtc
 val phe ala arg gly thr his gin ala ser gly leu gly asp val gly glu ala phe val
 181/61 211/71
 gag tcc ctt acc tcc cas gtt ggc ggg egg tcc act ggg gtc tac gca gtc gag acc tac cca
 asp ser leu thr ser gln val gly gly arg ser ile gly val tyr ala val asn tyr pro
 281/81 271/91
 gca aac gac gac tac cgc gcg aac gcg tca aac ggt tuc gat gat gtc aac gcc ccc atc
 ala ser asp asp tyr arg ala ser ala ser asn gly ser asp asp ala ser ala his ile
 301/101 331/111
 cag ccc aac gtc gcc aac tcc ccc aac aac aac atc gtc ctt ggt ggc tat tcc cag ggt
 gin arg thr val ala ser cys pro asn thr arg ile val leu gly gly tyr ser gln gly
 361/121 391/131
 ggc aac gtc atc gat ttg tcc acc tcc tgg atg ccc aac ggg gtc gtc gca gat met gtc gcc
 ala thr val ile asp leu ser thr ser ala met pro ala val ala asp his val ala
 421/141 451/151
 gct gtc gco ctt ttc ggg gag cca tcc aat ggt ttc tcc aat atg ttg tgg gyc gya ggg
 ala val ala leu phe gly glu pro ser ser gly phe ser ser met leu tpp gly gly gly
 481/161 511/171
 tcc ttg ccg aca att ggt cgg ctg tcc aat gtc tcc
 ser leu pro thr ile gly pro leu tyr ser ser lys thr ile asn leu cys ala pro asp
 541/181 571/191
 gat cca ata tcc aac gga ggc ggg aat att atg ggc cat gnt tcc tat gtt cgg tcc ggg
 asp pro ile cys the gly gly gly asp ile met ala his val ser tyr val gln ser gly
 601/201 631/211
 atg aca aac dag ggg ggg aca ttc ggg ggg aac aac aac ccc gat cac gca gga tgg
 met thr ser gln ala ala thr phe ala ala asn arg leu asp his ala gly CTA

SEQ ID N° 13D

FIGURE 13D

42 / 185

Seq13%: ORE prédicté par Cole et al. (1994) et comparé à l'ORE observé par Gosselin et al. (1994).

1/1
 tga ggc acg tca tgt ctc agg ggc cca tcc ucc act cgg tcc agc gca gta tgt cag cat
 OPA gly thr ser cys leu ser gly pro pro pro pso arg ser pro ala val cys gin his
 61/21
 91/31
 gtc cgg atg act cca cgc agg ctt gtt cgc atc gtt egt gtc gtc gtc gat gog acc acc ttg
 val gin met thr pro arg ser leu val cys ile val gly val val ala val cys gin his
 121/41
 131/51
 gcg ctg gtc agt gta ccc gcc ggc ggt egt dce ggc cat gcy gat cog tgc tgc gac atc
 ala leu val ser ala pro ala gly gly arg ala ala his ala asp pro mys ser asp ile
 181/61
 231/71
 gcg gtc gtc ttc gct agg ggc acc ccc cag gtc tct ggt ctt ggc gac gtc ggt gag gcg
 ala val val phe ala arg gly thr his gin ala ser gly leu gly asp val gly ala ala
 241/81
 271/91
 ttc gtc gac tcc ctt acc tcc cca gtt ggc ggg cgg tcc att egg gtc tac gcy gtc mac
 phe val asp ser leu thr ser gin val gly gly arg ser ile gly val tyc ala val asp
 331/101
 331/111
 tac cca gca agg gac gac tac agg gcy agg gog tca sac ggt tcc gat gat gtc ggc acc gco
 tyr pro ala ser asp asp tyr arg ala ser ser asn gly ser asp asp ala ser ala
 361/121
 391/131
 tac atc caq cgc acc gtc gcc agg agg tcc cgg ass acc egg att gtc ctt ggt ggc cat tcc
 his ala gln arg the val ala ser cys pro ass thr arg ile val leu gly gly tyr ser
 421/141
 451/151
 cag ggt gcg acg gtc acc gat gat ttg tcc acc tcc gcg atg agg ccc gcg gng gca gat cat
 gin gly ala thr val ile asp leu ser thr ser ala met pro pro ala val ala asp his
 481/161
 511/171
 gtc gca gat gtc gcc ctt ttc ggc ggg cca tcc agt ggt ttc tcc agg atg ttg tgg tgg ggc
 val ala ala val ala leu phe gly glu pro ser ser ser gly phe ser ser met leu trp gly
 541/181
 571/191
 ggc ggg tcc ttg ccc acc acc ggt agg ctt tat agg tct aag acc ata acc ttg tgg tgg gtc
 gly gly set leu phe thr ile gly pre leu tyr ser ser lys thr ile asn leu cys ala
 601/201
 631/211
 acc gca gat ccc ata tgt acc ggg ggc ggg set att arg gcg cat gtt tcc tat gtt csg
 pro asp asp pso ile cys thr gly gly gly ash ile met als Nle val ser tyr val gin
 661/221
 691/231
 tcc ggg atg acc agg cag ggg ggg acc ttc ggc gac sac agg tcc cat gtc gac ggg ggg
 sac gly maa thr ser gin ala ala alp thr phe ala ala sac arg ass his ala gca tpa
 691/231

13 of 13

FIGURE 138

43/185

31/11

CCA CGG GGG CTG CAG GGG CGA ATG TGC CGC GAA CGC CGT CGG CCA ACT TGG CGG CTG AGG
 pro pro gly leu glu gly arg met cys ala glu arg ser arg pro thr trp pro leu arg
 61/21
 91/31

GCG GCT GAT CCC CTG GCC CGA GAC GGG GCA AGC CAA TAG CGG CTC CAT CGG GCT TTG CTG
 ala ala asp pro leu ala arg asp gly ala ser glu AMB arg leu his arg ala leu leu
 121/41
 151/51

GTA GCG GTT CGG CGG GAA CGG AGC GCC GAC GGT GTC GGT CGC CGG TGA TAT ATT GGG TCA
 val ala val arg arg glu pro ser ala asp val val gly ala arg GFA tyr ile gly ser
 181/61
 211/71

GAC GGG TAT GUC GGC GAC TGA GGT GAT CTG CGA CAC GGC CGC GCG GTG CTC GAG CCA GGC
 asp gly tyr gly gly asp GFA gly asp leu arg his ala ala ala val leu glu pro gly
 241/81
 271/91

TTA CGA CCA GGG AAT TTC GAA AAT GTT ATT CAG ANC ATC TTG TAT CTU TTC CTC CGT GGC
 leu arg pro gly asn phe glu asn val ile gin asn ile leu tyr leu phe leu arg ala
 301/101
 331/111

ACE CGC TAG GTC TAG TGT TTT CGA GTA CGG GCA GAT CGC AGT TCA CGA GTC TCA CGA GAT
 thr pro AMB val AMB cys phe arg val pro ala asp pro ser ser pro val ser pro asp

C

SEQ ID N° 14A

FIGURE 14A

32/11

CAC CGG GGC TGG AGG GGC GAA TGT GCG CGG AAC CGC GTC GGC CAA CTT GGC CGC TGA CGG
 his arg gly trp arg gly glu cys ala pro asn ala val gly gin leu gly arg GFA gly
 62/21
 92/31

CGG CTG ATC CGC TGG CGC GAG AGG GGG CAA CGC AAC ATT AGC GGC TCC ATC GGG CTT TGC TGG
 arg leu ile phe trp pro glu thr gly gin ala asn set gly ser ile gly leu cys trp
 122/41
 152/51

TAG CGG TTC GGC GGG AAC CGA CGC CGG AGG TTS TCG CTG CGC GGT GAT ATA TTG GGT CAG
 AMB arg phe gly gly asn arg ala pro thr leu ser val pro gly asp ile leu gly gin
 182/51
 212/71

ACG GGT ATG CGG CGG ACT GAG GTG ATC TGC GAC AGC CGG CGG CGG TGC TCG AGC CGG GCT
 thr gly met ala ala thr gin val ile cys asp thr pro phe arg cys ser ser gin ala
 242/61
 272/71

TAC GAA CGG ATT TCG AAA ATG TTA TTT AGA ACA TCT TGT ATC TCT TCC GTG CGA
 tyr asp gin gly ile ser lys met leu phe arg thr ser cys ile ser ser ser val pro
 302/101
 332/111

CGU CCT AGG TGT AGT CTT TTC GAG TAC CGG CGG ATC CGA GTC CAC CGG TCT CAC CGG ATC
 pro phe arg cys ser val phe glu tyr arg gin ile pro val his gin ser his gin ile

SEQ ID N° 14B

FIGURE 14B

44/185

33/11
 ACC GGG GCT GGA GGG GCG AAT GTG CGC CGA AGC CCG TCG GGC AAC TTG GCC CCT GAG GGC
 thr gly ala gly ala asn val arg arg thr pro ser ala asn leu ala ala glu gly
 63/21 93/31
 GGC TGA TCC CCT CGC CGG AGA CGG GGC AAG CCA ATA GCG CCT CCA TCG GGC TTT GCT GGT
 gly CEA ser pro gly pro arg arg gly lys pro ile ala ala pro ser gly phe ala gly
 123/41 153/51
 AGC GGT TCG CGG GGA AGC GAG CGG CGT TGT GGG TGC CGG GTG ATA TAT TGG GTC AGA
 ser gly ser ala gly thr glu arg arg arg cys arg cys pro val ile tyr trp val arg
 183/61 213/71
 CGG GTA TGG CGG CGA CTG AGG TGA TCT GCG AGA CGC CGG GGT GCT CGA GGC AGG CTT
 arg val trp arg arg lys leu arg GPA ser ala thr arg arg arg gly ala arg ala arg leu
 243/81 273/91
 ACG ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT CTT GTA TCT CTT CCT CGG TGC GAC
 thr thr arg glu phe arg lys cys tyr ser glu his leu val ser leu pro pro cys his
 303/101 333/111
 CCC CTA GGT GIA GTG TTT TCG AGT ACC GGC AGA TCC CAG TTC ACC AGT CTC ACC AGA AGA TC
 pro leu gly val val phe ser ser thr gly arg ser gin phe thr ser leu thr arg

SEQ ID N° 14C

FIGURE 14C

partie de la séquence nucléotidique de seq14A

1/1 31/31
 TTT TCG AGT ACC GGC AGA TCC CAG CTT CAC CAG GTC TCA CGA GAT C
 phe ser ser thr gly arg ser gin val his gin val ser pro asp

SEQ ID N° 14A'

FIGURE 14A'

1/1 31/11
 TGT TTT CGA GTC CGG GCA GAT CGC AGG TTC ACC AGG TCT CAC CAG ATC
 cys phe arg val pro ala asp pro arg phe thr arg ser his gin ile

SEQ ID N° 14C

FIGURE 14C

1/1 31/11
 GTT TTC GAG TAC CGG CAG ATC CGA GGT TCA CGA GGT CTC ACC AGA TC
 val phe glu tyr arg gin ile pro gly ser pro gly leu thr arg

SEQ ID N° 14C'

FIGURE 14C'

FEUILLE DE REMPLACEMENT (REGLE 26)

45/185

ORF prédicté d'après la séquence publiée par Cole et al. (Nature 393:537~544) et
contenant seq14A'

1/1 31/11
 TAG CGG TTC GCG CGG AAG CTA GCG CGG ACG TTS TCG GTG GCC GGT GAT ATA TTG GGT CAG
 AMB arg phe gly gly lys leu ala ala thr leu ser val ala gly ser ile leu gly gln
 61/21 91/31
 ACG GGT ATG CGG CGC CCT GAG GTG ATC TGC GAC ACG CGG CGG CGG TGC TCG AGC CAG GGT
 thr gly met ala ala ala glu val ile cys asp thr pro pro arg cys ser ser gln ala
 121/41 151/51
 TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TTT TGT ATC TCT TCT CCG TGC CAC
 tyr asp gln gly ala ser lys met leu phe arg arg thr ser cys ile ser ser pro cys his
 181/61 211/71
 CCC CTA GGT GTA GTG TTT TCG AGT ACC CGC AGA TCC CAG GTT CAC CAG GTC TCA CCA gat
 pro leu gly val val phe ser ser thr gly arg ser gln val val his gln val ser pro asp
 241/81 271/91
 cca cgg ggc gcg atg asc ttc ccc gca tcc gca tcc ggt cca cgg cgg acg tgg tgg tgg ccc
 pro asp gly ala met asn phe pro ala ser ala ser pro gly arg arg arg thr trp ser arg
 301/101 331/111
 tat gag cgg aat ctg gag cct tgt cgg gca gca cat atc gaa gat gca ata ctt gag
 tyr asp gly asn leu gln pro cys arg ala ala gln his ile gln asp ala leu leu gln
 361/121 391/131
 tcc ttg cca gat cct gtc aga ttc ccc att tcc gca aag gag cgg tgg taa gcc cat gag cgt
 ser leu pro asp pro val arg phe pro ile ser ala lys glu arg tyr ala his asp arg
 421/141
 gag cgt tta cat taa
 asp arg leu his OCH

SEQ ID N° 14F

FIGURE 14F

45/185

Séquence RV3054c prédictée par Cole et al. (Nature 393:537-544) pouvant être en phase avec SsgIsh¹

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l/l 31/11
gtg tca gat acc sag tcc gac atc aac att ttg gcc tta gtg gga aac ctg cgc qcg qcg
val ser asp thr lys ser asp ile lys ile leu ala leu val gly ser leu arg ala ala
61/21 91/31
tgt ttc aac cgg cag atc gac gag ctg gct gcc aag gtc get cgg gac ggc gtc acc gtc
ser phe asn arg gin ile ala glu leu ala ala lys val ala pro asp gly val thr val
181/41 181/51
acc atg ttc ggg ggg ctg ggg gac ctg cgg ttc tcc sac gaa gac atc gac acc gcg acc
thr met phe glu gly leu gly esp leu pro phe tyr asn glu esp ile esp thr ala thr
181/61 211/71
gag gtg ccc ggg ccc gtg aac ggg ttg cgg gag gac ggg gag tct gac ggg cac get gac gac
glu val pro ala pro val ser ala leu arg gla ala ala ser asp ala his ala ala leu
241/81 271/91
gtg gtc acc ccc gaa tac sac ggc aac att ccc gca gtg atc aag sac ggg atc gac tgg
val val thr pro glu tyr ASN gly ser ile pro ala val ile lys ASN ala ile ASP trp
301/101 331/111
ctg tcc agg cca ttc ggc gat ggc ggg ttg aag gtc aag ccc ttg gca gtt gtc acc ggc ggg
ileu ser arg pro phe gly esp gly ala leu lys esp lys pro leu ala val ile gly gly
361/121 391/131
tcc atg ggc ccc tac ggc ggg gta tgg gcg cac gag gag act ccc aag tcc ttc aac atc
ser met gly arg tyr gly gly val tir ala his esp glu thr arg lys ser phe ser ile
421/131 451/151
gtt ggc acc cgg gtt gtc gat ggg atc aac ctg tcc gtg ccc ttc caa act ccc ggg aag
ala gly thr arg val val esp ala ile lys leu ser val pro phe glu thr leu gly lys
461/161 511/171
tgt gtc ggg gac gac gcc ggg ctg ggg ggg aat gtc cgg gac gac gtc ggc acc ttg gcc
ser val ala esp esp ala gly leu ala ala ASN val arg esp ala val gly ASN leu ala
541/181
gtt ggg gtc ggc tgg
ala glu val gly OPA

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SEQ ID N° 142

FIGURE 14B

47/385

ORF prédicté par Code et al. (2007) et portant le nom de

taa cgc gat cgg aat aax tcg gac cat ggt ccg gtt ggc tcc tgc aag gac gtg gac caa
 OCH arg asp arg ash lys ser asp his gln phe val gly ser mts lys asp val asp gln
 61/21 31/11
 91/31
 cca gog gaa agg aac gta gca gtg tcc gat acc aag tcc gac att aas atc ttg gcc tta
 gln ala glu arg ash val ala val ser asp thr lys ser asp ile lys ile leu ala leu
 121/41 151/51
 gtg gga agc ctg cgc gcg gcg ttc aac cgc gag atc gcc gag stg gct gac agg gtc
 val gly ser leu arg ala ala ser phe asn arg gln ile ala glu leu ala ala lys val
 181/61 211/71
 get ccc gac ggc gtc acc gtc acc atg ttc gag egg ctt ggg gac ctt ccc ttc tac aac
 ala pro asp gly val thr val met phe glt gly leu gly asp leu pro phe tyr asn
 241/61 271/91
 gaa gag atc gac acc gcg aag gaa gtc acc gtc acc gtc ctt ggg gac gtc ccc ttc tac
 glu asp lle asp thr ale thr glu val pro ala pro val ser ala leu arg glu ala ala
 301/101 331/111
 tct gac ggg gac get gac ttg gtg gtc acc ccc gac tac acc ggc aco att ccc gcc gtc
 ser asp ala his ala ala leu val val thr phe glu tyr asn gly ser lle pro ala val
 361/121 391/131
 atc aag aac gcy atc gac tgg ctt tcc agg ccc ttc ggc gat ggc gcy ttg aag gac aag
 ile lys asn ala lle asp trp leu ser arg pro phe gly asp gly ala leu lys asp lyc
 421/141 451/151
 ccg ttg gcc gtg atc ggc ggc tcc atg ggc ccc tac ggc egg gta ttg gcy ccc gac gac
 pro leu ala val lle gly gly ser met gly asp tcc tyr gly gly val trp ala his asp glu
 481/161 511/171
 act ccc aag tgg ttc aac atc gct ggc acg egg gtp gtc gat gcy atc aac ctc tgg gtc
 thr arg lys ser phe ser lle ala gly thr arg val val asp ala lle lys leu ser val
 541/181 571/191
 ccg ttc cca act ctc ggc aag tcc gtc ggc gac gac gtc gtc aag ctc gcc gcc aat gtc cgc
 pro phe gln the leu gly lys ser val ala asp arg ala gly leu ala ala asn val arg
 601/201 631/211
 gac gac gtc ggc aac ttg gcc gct gac ggc ggc tga
 ser ala val gly asp lle ala ala glu val ala OPA

SEQ ID N° 14P

FIGURE 142

48/185

fragment d'après la séquence publiée par Cole et al. (Nature 393:537-544) et contenant
seq 14F' et seq 14F'

1/1

31/11

caa cgc gat cgg aat aas tcc gac cat qgt ccc gtt ggc tcc tgg aag gac qtg gac cas
GCH arg asp arg asn lys ser asp his gly pro val gly ser cys lys asp val asp gln
asn ala ile gly ile asn arg thr met val arg leu ala arg als arg thr trp thr asn
thr arg ser glu OCH ile gly pro trp ser gly trp leu val gln gly arg gly pro thr
61/21 91/31

caa cgc gaa agg asc gta gca gtc tca gat acc aag tcc gac att aas atc ttg gcc tta
gln ala glu arg asn val ala val ser asp the lys ser asp ile lys ilis leu als leu
lys arg tla gly thr AMB gly cys gln ilis pro ser the ser lys ser trp pro AMB
ser gly lys glu arg ser val arg tla gly trp leu gln val arg his gln asn leu gly leu ser
121/41 151/51

gtg gga agc ctg cgc gcg gcp tcc atc cgg deg atc gcc qsg ctg gct gcc aeg gtc
val gly ser leu arg ala als ser phe amn arg gln ilis als glu leu als ala lys val
trp val als cys ala arg arg ser thr ala arg ser pro ser trp leu pro arg arg
gly lys pro ala arg gly val gln pro pro asp arg arg als gly cys gln gly arg
181/61 211/71

gtt cgg gag ggh gtc acc gtd acc atg ttc gag ggg gca gac ttg gag acc gtc acc ttc tac acc
ala pro asp gly val the val thr met phe glu gly leu gly asp leu pro phe tyr asn
leu arg thr ala ser pro ser pro cys ser arg gly trp gly thr cys arg ser the thi
ser gly arg arg his arg his val arg gly als ala gly pro ala val leu gln arg
211/71 271/81

gat cgg gag acc gca acc gcg amg gaa gtc gty cgg gag ccc gca gaa gca ttc cgg gag gac ggg
glu arg ala asp the ala the glu val pro ala val ser ala leu arg glu als als
lys the ser the gln arg arg cys arg cys arg arg GCA als arg cys gly arg pro arg
arg his arg his ser asp gly gly als ala gly glu arg val als gln gly arg val
301/101 331/111

tct gac gcg cac gct gca ttg gtc acc cgg gag tac asc ggc acc att ccc gca gtc
ser asp als ala als als leu val val the pro gln tyr als gln ser ilis pro als val
leu thr arg the leu pro trp tip ser arg arg asp the thr ala als phe arg pro GCA
GPA arg als arg cys leu gly gly his ala gly ilis gln arg gln his ser gly arg asp
361/121 381/131

ata aag hac gca acc gac tgg ctg tcc aag ccc ttc ggc yst egg gog gtc ttg eag gac aag
the lys asn als ile asp trp leu ser asp pro phe gly asp gly als leu lys asp lys
ser arg thr arg ser the gly cys pro gly his ser als met als asp GCA arg thr ser
gln als arg asp arg leu als val gln als als gln arg arg trp arg val gln gly gln als
421/141 451/151

cgg trp gac gng als gpc gdc tcc atl gtc aag ccc tac gyc ggg gta ttg ggg tac tac gac gag
pro leu als val als gly gly ser met gly arg tyx gly val trp als his asp glu
arg trp pro GCA ser als als pro trp als als the ala gly tyr gly arg thr arg
val gly arg asp arg arg leu his gly pro leu arg arg gly met gly als arg arg asp
481/161 511/171

act cgg aag tcc ttc acc acc get ggc acc gtc gtc get ggc acc aas ctc tcc tgg
thr arg lys ser phe ser ile ala gly the val val val als als lys leu ser val
leu als ser arg ser als ser leu als als gln gly trp ser met arg ser asn cys arg cys
ser gln val val gln his arg trp his ala gly gly arg arg cys asp gln the val gly als
541/181 571/191

cgg ttc cca act ctg ggc acc tgg otc gag gac gac ggg dtg gug gog gat gys cgg
pro phe gln the leu gly lys ser val als asp als gly leu als als asn val arg
arg ser lys leu trp als ser arg ser arg the thr pro gly trp arg dtg met cys als
val pro asn ser gly gln val gly arg gly arg arg arg als gly gln cys als als arg
601/201 631/211

gac gco gtc ggc acc ttc gco get ggg gtc ggg tcc tgg cgg gca ggg ggg ggg tcc gco
asp als val gly asn leu als als glu val gly GPA ser leu gly arg gly gln ser als
the pro ser als the tpp pro leu arg ser als asp pro trp als gln als gly gln pro
arg arg arg gln leu gln arg arg GCA gln arg als leu ilis phe gly pro arg arg val ser gln
661/221 691/231

ast aag ggc tcc atc ggc tcc gct ggt acc ggc ggt tcc ggg gca acc tcc cgg cpa nct tot
asn ser gly ser ile gly phe als gly ser als gly ser AMB arg arg arg cys
ile als als pro ser als leu leu val als val arg arg gln als ser gly asp val val
AMB arg leu his arg leu cys trp AMB arg phe gly gly gln lys leu als als thr leu ser

SEQ ID N° 14Q

FEUILLE DE REMPLACEMENT (REGLE 26)

49/185

781/241

781/251

cgg tgg cgg gtc ata tat tgg gtc aya cgg gta tgg egg cgg ctt agg tga tct ggg aca
 arg trp pro val ile tyr trp val arg cgg val trp arg arg leu arg CTA ser ala thr
 gly gly arg CTA tyr ile gly set asp gly tyr gly gly gly CTA gly asp leu arg his
 val ala gly asp ile leu gly gln thr gly met ala ala ala gln val ile cys asp thr
 781/261 811/271

cgc cgc cgc ggt gct cga gcc egg ctt acc acc agg gas ttt cga eas tgt tat tca gas
 arg arg arg gly ala ala arg ala arg ieu thr thr gly phe arg lys cys tyr ser glu
 ala ala ala val leu glu pro gly leu asp pro gly amn phe glu asn val his gln amn
 pro pro arg cys ser ser gln ala tyr asp gly ile ser lys met leu phe arg thr
 941/281 811/291

cet ctt gta tct ctc ctc cgt gcc acc ccc tag gng tag tgg ttt cga gta ccc gca gat
 his leu val ser leu leu ser ala thr AMB AMB AMB cys phe arg val pro ala ile
 ile leu tyr leu phe ser val pro pro pro arg cys set val phe glu tyr arg gln ile
 ser cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser
 901/301 811/311

coc agg ttc acc agg tct ctc cag ata cac ggg ggg cga tga act tcc cgg cat egg cat
 pro arg phe thr arg ser his gln ile his gly ala arg CTA thr ser arg his arg his
 pro gly ser pro gly leu thr arg ser the gly arg asp glu leu pro gly ile gly ile
 gln val his gln val ser asp pro arg gly ala met amn phe pro ala ser ala ser
 561/321 811/331

cpo cag gtc gaa gga cgt ggt arg cgt arg gga eas tgg aco ctt gtc ggg cgg ctc
 arg gln val asp gly arg arg ala met the gly ile trp ser leu val gly pro leu
 ala arg ser the asp val val ala leu CTA arg gln ser gly ala leu ser gly arg ser
 pro gly arg arg thr trp ser arg tyr arg gln amn leu gln pro rys arg ala ala gln
 1081/341 1051/351

sad ata tcc aag atg ccc tac tgg aat cgt tgg mag aac ctg tca gat tcc cga ttt cog
 asn ile ser lys met his tyr leu ser arg cys gln ile leu ser asp ser arg phe pro
 thr tyr arg arg cys thr the CTA val val ala arg ser cys gln ile pro asp phe arg
 his ile gln asp ala leu leu gln ser leu pro asp pro val arg phe pro his ser ala
 1081/351 1111/371

caa agg aag ggt acg ccc atg aac gtc aac gtt tac act aa
 gln arg ser gly thr pro met the val thr val tyr thr
 lys gly ala val arg pro CTA pro phe thr leu
 lys gln arg tyr ala his asp arg asp arg leu his CCA

SEQ ID N° 14Q(suite)

FIGURE 14Q(suite)

1/1

811/1

CAA GCC CGG CGG CGA CTG TTT GGC GTT TTG GGG CTC CTA CCA GAA CAC CAC CTG GCG CCC
 gln ala arg pro arg leu phe ala val leu gly leu leu pro glu his his leu ala ala
 61/21 811/21

CGC CAC CAT GGT GTG CAC CAG TTG CGA TCC GTT CCT CCC GCG CCC GGG CCG CGA CCA CCT
 ala his his gly val his gln leu arg set val pro phe ala arg gly arg arg arg arg
 131/41 151/51

CGA TGC CGG CGC CCC GGT GCG GCA CCT GCG TAG CTC GAC CGG GAC GAC GAC GCG GTC
 arg cys pro arg pro gly gly ala ala ala AMB leu esp pro val esp esp esp gly val
 181/61 211/71

GCG GGA CCA GTC GGC GAT GTC GAG GCG ATG GCA ATA CAG CGG CTT GGT GCG CGG CCA CAC
 gly gly pro val gly asp val gln ala met ala ile gln arg leu gly ala arg pro his
 241/81 271/91

GTC TGA GGT GGC GAA GAC CAG TCC CGC GCG GCG CAG CAG CCG GAT CGG GAT AGG CGG TAC
 val CTA gly gly glu esp gln ser arg ala his arg gln pro esp pro esp the arg tyr

SEQ ID N° 15A

FEUILLE DE REMPLACEMENT(REGLE 26)

50/185

32/11

AAG CCC GGC CSC GAC TGT TTG CGG TTT TGG GGC TCC TAC CAG AAC ACC ACC ACC TGG CGG CGS
 lys pro gly arg asp cys leu pro phe trp gly ser tyr gln asn thr thr trp arg pro
 62/21
 CGC ACC ATG GTG TGC ACC ACT TGG GAT TTC CTC CGG CGC CGG GGC GGC GAC GAC GTC
 arg thr met val cys thr ser cys asp arg phe leu pro arg ala gly gly asp asp val
 122/41
 152/31
 GAT GCC CGC CGC CGG CGG CGA CTG CGT AGC TCG ACC CGG TCG ACG ACG ACG CGG TCG
 asp ala arg ala pro ala ala gln leu arg ser ser thr arg ser thr thr gly ser
 182/61
 212/71
 GCG GAC CAG TCG GCG ATG TCG AGG CGA TGG CTA TAC AGG GCG TTG GTG CGC CGC CAO ACC
 ala asp gln ser ala met ser arg arg trp gly tyr ser ala leu val arg gly His thr
 242/81
 272/91
 TCT GAG GTG CGG RAG ACC ATG CGG CGC ACC CGC ACC CGG ATC CGG ATA CGC CGT AC
 ser glu val ala lys thr ser pro ala pro thr gly ser arg ile arg ile arg gly

SEQ ID N° 15B

FIGURE 15B

33/11

AGC CGG ACT GCG ACT GTT TGC CGT TTT CGG GCT CCT ACC AGA ACA ACA CGA CGC CGC CGC CGC
 ser pro ala ala thr val cys arg phe gly ala pro pro the arg thr pro pro gly gly arg
 63/21
 83/31
 GCA CCA TGG TGT GCA CCA GTT CGG ATG GGT TCC TCC CGG CGC CGG CGC CGC CGC AGC AGC TCG
 ala pro trp cys ala pro val ala ile gly ser ser arg ala arg ala ala thr ser
 123/41
 153/51
 ATG CGC GCA CGC CGG CGG CGC AGC TGG GTA CCT GCA CGG CCT TGA CGA CGA CGG CGT CGG
 met pro ala pro arg arg arg ser cys val ala arg phe gly arg arg arg arg gly arg
 183/61
 213/71
 CGG ACC ACT CGG CGA TGT CGA CGG GAT GGC ATT ACA CGG CCT TGG TSC CGG CGC CGC ACA CGT
 arg thr ser arg arg cys arg gly asp gly asn the ala pro trp cys ala ala thr arg
 243/81
 273/91
 CTG AGG TGG CGA AGA CCA GTC CGG CGC CGA CGG CGA CGG TGG CGA TAC CGG GTA C
 leu arg trp arg arg pro val pro arg pro pro ala ala gly ser gly tyr ala val

SEQ ID N° 15C

FIGURE 15C

51/185

partie de la séquence nucléotidique de seq15A

1/1 31/11
 GGC GGC CGC CGG CCA TGG TGT GCA CCA GTT CGG ATG GGT TGT CCC GCG CGG CGG CGA
 gly gly arg ala pro trp cys ala pro val ala ile gly ser pro ala arg gly arg arg
 61/21 91/31
 CGA CGT CGA TGG CGG CGG CCC GGC GGC TGC AGC TGC GTC GCT CGA CGG CGT CGA CGA CGA
 arg arg arg trp pro arg pro gly cys ser cys val ala arg pro gly arg arg arg
 121/41 151/51
 CGG GGT CGG CGG CGG ACT CGG CGA TGT CGA CGG GAT GCG AAT ACA GCG CCT TGG TGC CGG
 arg gly arg arg ala ser arg arg cys arg gly asp gly asn thr ala pro trp cys ala
 181/61 211/71
 GCC AGA CGT CTG AGG TGG CGA AGA CGA GTC CGG CGG CGA CGG CGA TC
 ala thr arg leu arg trp arg arg pro val pro arg pro pro ala ala gly

SEQ ID N° 15A'

FIGURE 15A'

1/1 31/11
 GCG GTC CGC CGC CAT GGT GTG CAC CAG TTC CGA TGT CGT CGG CGG CGG CGC GAC
 ala ala ala arg his gly val his gln leu arg ser val leu pro arg ala gly gly asp
 61/21 91/31
 GAC GTC GAT CGC CGC CGG CGG GCT GCA GTC GCG TAC CGT CGC GAC CGC GTC GAC GAC GAC
 asp val asp gly arg ala pro ala ala ala ala ser ASP pro val asp asp asp asp
 121/41 151/51
 GGG GTC CGC CGG CGA GTC CGG GAT GTC GAG CGG ATG CGA ATA CGG CGC CTT CGT CGG CGG
 gly val gly gly pro val gly asp val gln ala met ala ile gln arg leu gly ala arg
 181/61 211/71
 CGA CGC GTC TGA GGT CGC GAA GAC CGG TGC CGG CGU CGC CGG CGG GAT C
 gcu his val GPA gly gly glu asp gln ser arg ala din srg gln pro asp

SEQ ID N° 15B'

FIGURE 15B'

1/1 31/11
 TGG CGG CGC CGG CGC AAG GTC TGC ACC AGT TGG GAT CGG TTC TGC CGG CGG CGG CGG
 tryx arg pro arg ala met val cys thr ser cys asp ser the ser arg ala arg ala ala
 61/21 91/31
 AGC TCA ATG CGC CGG
 the RNC ser met ala ala pro arg arg leu gln leu arg ser ser the arg ser the Thr
 121/41 151/51
 AGG GGG TGG CGG
 thx gly ser ala gly gln ser ala met ser ser ser trp gln Tyr ser ala leu val arg
 181/61 211/71
 CGC CGC AGG TCT GAG GTG CGG AMG AGC AGT CGG CGG CGG CGG CGC AGG CGG ATC
 gly his thr ser gln val ala lys thr ser pro ala pro thr gly ser arg ille

SEQ ID N° 15C'

FEUILLE DE REMPLACEMENT (REGLE 26)

52/185

1/1
 taa ggt ccc cca acg att tac gct cgg cgg cca cca gtt ggc cgg cca cct tca ggc
 DCH gly pro pro thr leu tyr ala arg pro pro arg val gly arg pro leu ser gly
 61/21
 51/31
 cgt agt ccc ccc agg gca egg ctt acc ggg tcc tgg cgg gtt tgg cgg cca agg tgg
 arg ser arg arg arg ala gly leu pro ala ser ser ser arg val sys arg gin arg cys
 121/41
 151/51
 agg ggt agc gct cgt cgg cgg cga cga tgg gca gtc cgg gca tgg cgg cgg cgg cgg
 arg gly ser val arg gly arg arg arg arg cya cya ala ala arg gly cys arg arg arg gly
 181/61
 211/71
 cgg tgg ggg tgg gca ccc ccc ggg act gtt tgg tgg cgg tct tgg ggg tct gat ggg
 arg trp gly cys ala arg phe ala ala thr val cys ala phe trp gly ser ala arg thr
 241/81
 271/91
 cca cct ggc ggc ccc ggg cca tgg tgg gca cca gct ggg aac ggt tct ccc ggg ccc ggg
 pro pro gly gly arg ala pro tgg cys ala pro val ala ile gly ser pro ala arg gly
 301/161
 331/171
 cgg cpa cga cgg cys tgg cgg cgg doc ygg ggg tgg sec sec tgg gta gct cga ccc ggt cpa
 arg arg arg arg arg trp pro arg phe gly gly cys sec cys val ala arg pro gly arg
 361/212
 391/181
 cga cga cgg cgg cgg wgg
 arg arg arg gly arg arg ala ser arg arg arg cys cys cys gly asp gly asp thr ala phe trp
 421/141
 451/181
 tgg ggg gcc aca cgt ctg agg tgg cgg cgg cgg aat aat aat aat aat aat aat
 cys ala ala thr arg leu arg trp arg arg pro val pro arg pro phe ala ala gly ser
 481/161
 511/171
 ggt agg gca ggc ggg agr ctt cag cgg ggt tgg cgg cgg cgg cgg cgg cgg cgg
 gly arg ala gly ala ser leu gln arg gly trp arg arg arg ala ala pro gln ser val
 541/181
 571/181
 agg gta cgg cgg cgg cgg tcc ggg aac ggt gaa gca ggg aat nnn agg aac aac cca tgg tcc cgg
 arg val arg ala ala tyr gly asn gly gln ala gly che phe thr asn pro ser ser arg
 601/201
 cga agg ggc agg tgg
 arg arg dly ala GCA

SEO TO N° 1 - 36

FIGURE 15

53/185

Rv2530c prédicté d'après Cole et al. (Nature 393:537-541) et pouvant être en phase avec SEQ15A

1/1 31/11
 gtg acg gca ctg ctc gat gtc aat gtg ctg atc ggg tgg ggc tgg cog aat cac gtt cac
 val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his val his
 61/21 31/31
 cat ggc gcc ggg cgg cca tgg ttc aac cag ttc tcc tcc aat ggg tgg ggc acc aac ccc
 his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr thr pro
 121/41 151/51
 att aca gag gca ggg tat gtc cga att tca aac aat ccc aat ggg atg gag ggg tgg tgg acc
 ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val ser thr
 181/61 211/71
 acy ccc gct atc gcg atc gct cag ttc ggg ggg atc act tat ctt gcc ggg cac acc ttt
 thr pro ala ile ala ile gln leu ala ala met thr ser leu ala gly his thr phe
 241/81 271/91
 tgg ccc gac gat gtc cca ctg atc gtt ggg aac ggc ggg gat ccc gat ggg gtt tcc aac
 trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp als val ser asn
 301/101 331/111
 ccc cgt cgg gcc acc gca tgg cat ctc aac gcc tgg gcc ccc ccc taa ggg ggc ccc tgg
 his arg arg val thr asp cys his leu ala ile leu ala ala arg tyr gly gly arg leu
 361/121 391/131
 gtc aca ttc gat gcc gca tgg gca get tca gca tcc gca gpc ctc gtc gag gtg tgg tag
 val thr phe asp ala ala leu ala asp ser ala ser ala gly ile val val gln val leu AMB

SEQ ID N° 15R

FIGURE 15R

Seq15P: ORF d'après Cole et al. (Nature 393:537-541) contenant Rv2530c

1/1 31/11
 tgg tgt tcc gcc gga tyc gcc gac ggt gac ttc cga gga tgt cgt ccg ccc gct cgg ggg
 GFA cys ser ala gly cys ala asp gly asp phe arg gly cys arg pro arg ala arg gly
 61/21 91/31
 cgg cgt cgg aac gca ctg ctc gat gtc aat gtc ctc atc gcy ccg ggg tgg cog aat cac
 arg arg val thr ala leu leu asp val asn val ile ala leu gly trp pro asn his
 121/41 151/51
 gtt cat gat ggg gcc ggg cay cga tgg ttc aeg ccc tcc tcc tcc aat ggg tgg gcc aac
 val his his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr
 181/61 211/71
 aag ccc att acc gag gca ggg tcc gtc cga att tcc aac aat ccc aat gtt atg ccc ggg
 thr pro ile thr gln ala gly tyr val arg ile ser ser asn arg ser val met gln val
 241/81 271/91
 ccc acc aac ccc gac aac ggg tcc gtc cga att tcc aac aat ccc aat gtt atg ccc ggg
 ser thr thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his
 301/101 331/111
 acc ttt tgg ccc gac gat gtt ggg cca ctc aac gtc ggg aac gca ggg gat ccc aat gcy ggg
 thr phe trp pro asp asp val pro ile ala val gly ser ala gly asp arg asp als val
 361/121 391/131
 tcc aac ccc cgt ccc gtc acc gac tgg aat ctc aac gcc tgg gcc ggg ccc tac ggg gpc
 ser asn his arg arg val thr asp cys his leu ala ile leu ala ala arg tyr gly gly
 421/141 451/151
 egg tgg gtc acc ttc gat gcc gca tgg gac gat tca gca tcc gca ggg ctc gtc gag gng
 arg leu val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val gln val
 481/161
 tgg tgg
 leu AMB

SEQ ID N° 15P

54/185

Fragment contenant Seq15F' et Seq 15F'

1/1 31/51
 tga tgt tcc gco gca tgc gcc gac ggt gac ttc cga gga tgt cgt ccc ggg gct cga gga
 GFA cys ser ala gly cys ala asp gly asp gne arg gly cys arg pro arg ala arg gly
 asp val pro arg ala pro thr val thr ser glu asp val val arg ala leu glu asp
 Met phe arg arg met arg arg arg GFA ser pro arg met ser ser ala arg ser arg thr
 61/21 91/51
 cys cgt cgg acc gca ctc gag act gtc act gtc stg act gcy ctg ggc tgg ccc act cac
 arg arg val thr ala leu leu asp val val leu ala leu gly trp pro asp his
 asp Val GFA arg has cys ser met met met cys GFA ser arg trp ala gly arg ile the
 thr cys asp gly thr ala arg cys gin cys ala asp arg ala gly leu ala glu ser arg
 121/41 151/51
 gtt cat mat gcg gco gog cag cgy tgg ttc arg bag ctc tcc bat egg bat egg gco acc
 val his his ala ala ala ala arg trp phe thr the gin phe ser ser asp arg trp ala
 phe thr met arg pro arg sex asp gly set arg ser ser pro arg met gly gly pro pro
 ser pro cys gly arg ala ala met val his ala val leu glu trp val gly his his
 181/61 211/71
 acg ccc acc acc gag gca ggg that gtc cga att tcc arg asp cgo cgt cgg atg cag cug
 thr pro ile the gin ala gly tyr val arg ile ser ser asp arg val met gin val
 arg arg ser pro arg gin gly met ser glu phe gin ala ile ala val GFA cys arg cys
 ala asp his arg gly arg val cys pro amn phe lys gin seg gin cys asp ala gly val
 241/81 271/91
 tag acc acc ccc act arg gco act get cag ttg gco gog arg acc act ctt gco ggg ccc
 ser thr thr pro ala ile ala ile ala gin leu ala ala met thr ser leu ala gly his
 arg pro arg arg ala ser arg ser leu sex trp arg arg GFA leu leu pro gly thr
 asp his ala gly tyr arg arg ser val gly gly asp asp phe ser cys arg ala his
 301/101 331/111
 acg ttt tag ccc gac gag gtg ccc act ctc act ggg arg gco gag act ccc gag
 thr phe trp pro arg asp val pro leu ala val gly ser ala gly asp arg asp ala val
 arg phe gly leu thr met cys his GFA ser leu gly ala pro ala ile ala met arg cys
 val leu ala GFA arg cys ala thr asp arg trp glu arg arg ser arg cys gly val
 361/121 391/131
 tcc acc cac cgt cgg act acc gag tgc cat ctc act gcc tcc tgg gco ggg ccc tac ggg gco
 ser his has arg arg val thr asp cys his leu ala ala ala ala arg tyr gly gly
 pro thr thr val gly ser pro thr ala ile ala ser ser pro trp pro arg ala the gly ala
 gly pro pro ser gly his arg leu pro ser his arg leu gly arg ala leu arg gly pro
 421/141 451/151
 cgg ttg gtc aca the dat gco gca ctc gco gtc gat tca gca tcc gca gco ctc gco gag gty
 arg leu val thr phe asp ala ala ala asp ser ala ser ala gly leu val glu val
 gly trp ser his ser met pro his trp pro ile gin bin pro gin ala ser ser arg cys
 val gly his ile arg cys arg thr gly arg phe ser ile arg arg pro arg arg gly val
 481/151 511/171
 ttt tag tca ccc ggg arg gco gag ccc gtc cat gag cat stg cgg ggg cag gco ccc
 leu AMB ser pro gly met gly gly ser phe gly leu asp leu arg ala gin ala pro
 cys ser his arg gly trp ala ala arg gin ala cys arg ile cys gly arg arg arg pro
 val val thr gly asp gly arg leu ala his ala arg ser ser ala leu leu gly
 gly Arg thr phe ala gly arg arg phe trp pro thr arg ala ala arg cys trp ala
 541/181 571/191
 ccc gtc gga ccc cgg gag gtc gag got ttt gyc ccc act gco gag ctc gco gtc gat ggg
 pro val gly his arg gin ala asp ala phe gly pro arg ala gin leu gly ala ala gly
 arg ser arg thr gly arg pro thr leu leu ala his ala arg ser ser ala leu leu gly
 gly Arg thr phe ala gly arg arg phe trp pro thr arg ala ala arg cys trp ala
 601/201 631/211
 ccc ggg ccc ggg acc cgg ctc gaa sed cgt ggt gco gtc gyc act gtc gag gca mon
 leu leu gly leu gly gly ser arg leu glu mon arg gly gly val gly ile val asp glu pro
 ser gly ser ala ala ala gly ser lys thr val val ala ser ser met thr son gin
 arg ala arg arg gin pro ala arg lys pro trp trp arg arg his arg arg arg thr arg

SEQ ID N° 15Q

FIGURE 15Q

FEUILLE DE REMPLACEMENT (REGLE 26)

153 / 200

661/221 693/231
gtt gag ggc ggc ggc tag ata gcg qta gct gta ttc ctg ggg gag ctt ggc ggt tgg gca
gag gtc gtc gly gly gly AMB llt ala val gly val phs leu gly glu leu ala gly leu ala
val arg ala ala ala ala arg AMB arg AMB val tyr ser trp ala ser leu arg val trp gln
GFA gly arg arg leu asp ser gly arg cys ile pro gly arg ala cys gly phe gly arg
721/231 781/251
gaa caa get cgg ccc gtc ggc ass gct gat ctg cas tcc gpc gac cod acc gtc gat met gtc
gaa his asp arg his val gly lys ala asp leu gln phe gly gln pro ile gly gln arg
ass thr lle gly the leu gly lys pro ile cys ass ser ala ser pro ser ala lle ala
Thr arg ser ala arg trp gln ser arg ser ala arg pro ala his arg arg ser pro
721/251 811/271
cgt cgg ggc gaa gga gtc gtc gac gat ctc cgs gta gng gtc ctc gac cas ccc gtc
arg arg ala gly glu gly val arg gln asp leu arg val ala val leu asp his his gly
val gly arg ala lys gln cys ass lys lle ser gln AMB arg met ser thr the thr ala
ser gly gly gln arg arg ser ala asp arg ser pro ser gln phe pro arg pro pro arg
811/281 871/291
ggc ccc tgg cag ccc ggc cag ttc gct ggt gta ttt ccc gtt gco gtt cag can gcc
gcy val pro trp gln arg gly gln phe gly gln leu val phe gln vsl ala val gln his ala
ala arg gly ser ala ala ser ser val ser trp phe phe arg leu pro phe ser the pro
pro val ala ala arg pro val arg ser val gly lle ser gln cys arg ser ala arg
811/301 831/311
aga egt asy gtc ccc cac ccc ttc aag ctc gac ggc ccc cac ggg tgg gcc gac ctt
arg ass lys val arg gln arg phe thr leu asp gly arg his gln leu ala gly his phe
gly val arg ser ala ccc ala leu arg ser thr the thr ser trp pro ala the phe
lys OCH gly pro pro pro thr leu tyn ala arg arg phe phe arg val gly arg pro leu ser
811/321 991/331
ggc gtc gtc gca gca ggg cag ggc tcc ccc ccc egt ctt ccc ggg ttt gtc ggc ass
gln ala val val ala ala ala gly gln phe pro arg arg leu arg gly phe val gly lys
arg pro AMB ser pcc gln gly arg sia ser arg val val phe ala gly leu ser ala lys
gly arg ser arg arg arg asp ala gly leu pro ala ser ser ser arg val cys arg gln arg
1031/341 1051/351
ggt gta ggg gta ggg gtc gtc gtc gac gac gat gtc gsg ctc gpc gat gtc ggc ggg
gly val gly val ala phs ala phe gly val asp asp ass vsl gln leu gly arg asp ala gly
val AMB gly AMB arg ser trp ala ala ser the the met cys ser ser gly met pro ala ala
cys arg gly ser val arg gly arg arg arg arg cys ala ala arg gly cys arg arg
1081/361 1111/371
ggc ggg ggt ggg ggt ggg ass gcc cgg ccc cga ctc ttt ggg cgt ttc ggg act ctc cca
ala gly gly gly ala his ala arg pro arg ala arg pro arg ala gly gln ala leu pro
arg ala val gly val arg the pro gly arg arg asp cys ias arg val leu gly leu cys gln
gly arg trp gly cys ala arg pro ala ala the val cys ala phe trp gly ser ala arg
1161/381 1171/391
gaa caa can ctc ggc ggc gpc gpc cat ggt gng dad amg ttc cga tcc gtt atc ccg ccc
gln his his leu ala ala ala arg his gly val his gln leu gln arg ser val leu pro arg
sen the thr trp arg pro arg ala met val cys thr ser cys arg arg phe ser arg ala
the pro pro gly arg arg ala pro trp cys ala pro val ala the gly ser pcc ala arg
1201/401 1231/411
ggc ggg gtc gac gac gtc gtc ggt ggg ccc god ccc god god god gtc gtc gac ccc
gln gly gly ass arg val arg gly val arg ala pro ala ala ala ala AMB leu asp arg
arg ala ala the thr ser met ala ala pro arg arg ieu gln leu arg ser ser the arg
gly arg arg arg arg arg trp phe phe arg pro gly gly cys ser cys val ala arg pro gly
1261/421 1291/431
gtt gca gtc
val asp arg arg gly val gly gly pro val gly val gly val gln ala met ala ala ala
ser the thr the gly ser ala gly gln ser ala met met ser arg arg trp phe phe ser ala
arg arg arg arg gly arg gln gln ser arg arg AMB ser gln gln gln gln gln gln gln

MCG 1B N° 160 (cont'd.)

FIGURE 250. (Continued.)

56/185

1321/441 1361/451
 ctt ggt ggg ccc ccc gtc tga ggt ggc gaa gac ccc tcc cpc gac ccc ccc
 leu val ala arg pro his val OPA gly gly glu asp glu ser arg ala his arg glu pro
 leu val arg gly his the ser gld val ala lys thr ser phe ala pro the gly ser arg
 trp cys ala ala thr arg lsa arg trp arg arg pro val pro arg pro pro ala ala gly
 1361/451 1411/471
 gat cag gta ggg gag ggg cya gtc ttc ayc ggg gtc gpc gac gac ccc ccc aga
 asp glu val gly glu ala arg val phe ser gly val gly asp glu glu leu his arg
 ile arg ASN gly arg arg glu ser ser ala gly leu ala ala thr ser ser ser the glu
 ser gly arg ala gly ala ser leu glu arg gly trp arg arg arg ala ala pro glu ser
 1441/481 1471/491
 gtc tga ggg tac ggg egg cgt egg gca ayc ggt arg ccc ccc ccc ccc ccc
 val OPA gly tyr gly arg arg thr ala the val lys gln ala leu arg arg the his arg
 cys glu gly thr the gly gly val arg gln arg OPA ser arg his ser asp glu pro ile val
 val arg val arg ala ala tyr gly ann gly glu ala gly thr pro thr ann pro ser ser
 1501/501
 ccc gtc gaa ggg gca ggt ga
 his val glu gly ala gly
 thr ser lys gly gin val
 arg arg arg gly arg OPA

SEQ ID N° 15Q (suite 2)

FIGURE 15Q (suite (2))

. 31/11
 TGC GCA TCC CGA CCA GTG TGG TTG GCC GAA GTT CCT TTG TTC GCG ATT GCC TCA AGG ATT
 cys ala cys arg pro val trp leu ala gly val arg leu phe ala ile ala ser thr ile
 41/21 31/31
 CGA TAT AAC TAC TCT ACT CAC ATC ARC ARC CAT ACT CCT ACC ATT GAG CCT GTG GGT TGA TGC
 arg tyr asn his sec ser his ile ann his the arg thr ile glu arg val gly ser cys
 121/41 131/51
 CAT GCA TTC CGG ACC GCG GGA GGC GGC GAA CCC CCC CCC CAT ATT CCA GRT TGA GCA
 his ala phe ala thr ala gly ala gly glu pro gly ala the his ann pro asp OPA gly
 181/51 211/51
 GAC TTC CGT CCC GAA CCG ACC CGG ACC CAA GCT TTC GAC AGC CAT GAG CGG GGT CGG CGC
 asp phe arg ala glu pro the phe thr glu ala phe asp ser his glu arg gly arg arg
 241/51 271/51
 CCT GGC AGT TGC AAC TCC TTG TGC ATA TTT TCT TGT CTA CGA ATC AAC CGA AAC GAC CGA
 pro gly ser cys lys ser leu cys ile phe ser cys leu arg ile asn arg ann asp arg
 301/101 331/111
 GCG CCC CGA CGA CGA TGA ATT CAA CGA GGC GGC CCT TTT GAC CGA CCT GGC CGG CGA CCT
 ala ala arg ala pro OPA ile gln ala gly gly gly val asp arg pro ala arg arg ala
 361/121
 GAT GTC CGC CCT ATC CGA GGG GTT GTC CGA GTT CGG CGG CAT C
 asp val arg ala ile ala gly val val val pro val arg asp

SEQ ID N° 16A

FIGURE 16A

57/185

32/11

GCG CTT GGC GAC CAG TGT GGT TCG CGG GAG TTC GTT TGT TCG CGA TTG CCT CAA CGA TTC
 ala his ala asp gln cys gly trp pro glu phe val cys ser arg leu pro gln arg phe
 62/21 92/31
 GAT ATA ACC ACT CTA GTC ACA TCA ACC ACA CTC GTC CGA TCG AGC GTG TGG GTT CAT GCG
 asp ile thr thr leu val thr ser thr leu val pro ser ser val trp val his ala
 122/41 152/51
 ATG CAT TCG CGA CGG CGG GAG CGG GAC CGG GCG CGA GAC ATA ATG CGG ATT TAG GAG
 met his ser arg pro arg glu pro ala asp pro ala pro his ile gln ile gln glu
 162/61 212/71
 ACT TCC GTG CGG AAC CGA CGG CGA CGG AAG CTT TCG ACA GCG ATG AGC CGC GTC CGC GUC
 thr ser val pro asp arg arg arg lys leu ser thr ala met ser ala val ala ala
 242/81 272/91
 CTC GCA GTT GGA AGT CCT TGT GCA TAT TTT CTT GTC TAC GAA TCA ACC GAA AGC ACC GAG
 leu ala val ala ser pro cys ala tyr phe val val tyr glu ser thr glu thr thr glu
 362/101 332/111
 CGG CCC GAG CAC CAT GAA TTC AAC CGG GUG GCG GTG TGG ACC GAC CTG CGC CGC GAG CTG
 arg pro glu his his glu phe lys glu ala ala val leu thr asp leu pro gly glu leu
 362/121 392/131
 ATG TCC CGG CTA TCG CAG CGG TTG TCC CGG TCC GAG ATC
 met ser ala leu ser gln gln leu ser gln phe gly ile

SEQ ID N° 16B

FIGURE 16B

33/11

CGC ATG CCG ACC AGT GTG GTT GGC CGG AGT TCG TTT GTT CGT SAT TGC CTC AAC GAT TCG
 arg met pro thr ser val val gln arg ser ser phe val arg asp cys leu asn asp ser
 83/31 83/31
 ATA TAA CGA CTC TAG TCA CAT CAA CGA CGC TCG TAG CGT CGA CGG TGT GGG TTC ATG CGA
 ile CGR pro leu RMB ser his gln pro his ser tyr his arg ala cys gly phe met pro
 123/41 153/51
 TGG ATT CGG GAC CGC GGG AGC CGG CGA AGC CCG CGC CGA AGA TAA TCC AGA TTG AGG AGA
 cys ile arg asp arg gln ser arg arg thr arg arg his thr CGH ser arg leu arg arg
 163/61 213/71
 CTT CGG TGC CGA ACC GAC CGC CGC CGA AGC TTT CGA CGG CGA TGA CGG CGG TCG CGG CGC
 leu pro cys arg thr asp ala esp ala ser phe arg gln pro GFA ala arg ser pro pro
 243/81 273/91
 TGG CGG TTG CGA GTC CTT GTG CTT ATT TTC TGG TCT AGG ATT CGA CGG AAA CGA CGG CGG AGG
 trp gln leu gln val leu val his ile phe leu ser thr asn gln pro lys arg phe ser
 363/101 333/111
 GGC CGG AGC ACC ATG ATT TCA AGC AGG CGG TGT TGA CGG AGC TGC CGG CGG AGC TGA
 gln pro ser thr met asn ser ser arg arg arg cys GFA pro thr cys pro ala ser GFA
 363/121 393/131
 TGT CGG CGC TAT CGG AGG GGT TGT CGG AGT TCG GGA TO
 cys pro arg tyr arg arg gln cys phe ser ser gln

SEQ ID N° 16C

FIGURE 16C

FEUILLE DE REMPLACEMENT (REGLE 26)

58/185

31/11

GCG GGC CAC CGA TCA GTC GAT CGG ATG GTT TCC GCT CGA TCA GCC CGG AAT TGA GGT GCG
 ala gly his arg ser val asp arg val val ser ala pro ser als arg arm OPA gly als
 61/21 91/31

GCA GTG ACG ACA CGA CGG CAG GRC GCG CGG TTS GTG TTT CCC TCT GTG GCT TTG CGG TCC
 als val thr thr pro als gln asp als phe leu val phe pro ser val als phe pro ser
 121/41 151/51

GGC TGG CCT TTT TTT CAT CAA CGT TGG ACT GGC GCA GTG GCG ATG TTS GTC GCG GCG GTG
 gly ser pro phe phe his gln arg trp thr ala als val als met leu val als gly val
 181/61 211/71

TTC GGT CAC CTG AGG GTC GGG ATG TTC CTT GGG TCT CGG GTT CCT GCT GCG AGG TTT GCT CAA
 phe gly his leu thr val gly met phe leu gly ser arg val als als gly phe als gln
 241/81 271/91

TGC CCT GCT GGT GCG GCG TTC GGC CGA GTC GAT CAC CGG CAA AGA GCA CGG CCT AAA ACK
 cys pro als gly als als phe gly arg val his arg gln arg als pro val lys thr
 301/101 331/111

GTC GAT GCG CCT CAA CTC GGC ATC GCG ACT GGC GAT TAT CGC CAT GCC TGG GCG TCA TC
 val esp gly phe gln leu gly ile als thr gly esp tyr his his als ser gly OPA

SEQ ID N° 17A

FIGURE 17A

32/11

GCG GCC ACC GAT CAG TCG ATC GCG TGG TTT CGG CTC CAT CGG CCT GGA ATT GAS GTG CGG
 arg als thr asp gln ser ile gly trp phe pro leu his gln pro gly ile glu val phe
 62/21 92/31

CAG TGA CGA CAC CGG CGC AGG AGG CGC CGT TGG TGT TTC CCT CGT TTG CCT TCC CGT CGG
 gln OPA arg his gln arg arg thr arg arg trp cys phe pro leu leu ser arg pro
 122/41 152/51

GCT CGC CTT TTT TTC ATC AAC GTT GGA CTC CGG CAG TGG CGA TGT TGG TCG CGG TGT
 als arg leu phe phe ile asn val gly leu pro gin trp arg cys trp ser phe als cys
 182/61 212/71

TCC GTC ACC TGA CGG TGG GGA TGT TCC TGG GGT CTC GGG TGG CGT CGT CGG GGT TTG CTC AAT
 ser val thr OPA arg ser gly cys ser leu gly ile gly leu leu gly ile leu asp
 242/81 272/91

GCG CTC CTC CGG CGT TCG GCC GAG TGG ATC ACC GCG AAA GAG CAC CGG TTA AAA CGG
 als leu leu val arg ser als gln ser ile thr als lys glu his pro leu lys arg
 302/101 332/111

TGG ATG CGC CTC AAC TCG GCA TCG CGA CTC CGG ATT ATC ACC ATG CCT CGG CCT GAT C
 ser met als leu asp ser als ser arg leu als ile ile thr met phe arg als asp

SEQ ID N° 17B

FIGURE 17B

59/185

33/11

GGG CGA CGG ATC AGT CGA TCG GGT GGT TTC CGG TCC ATC AGG CGG GAA TTG AGG TCC CGC
 gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro glu leu arg cys arg
 63/71 93/31

AGT GAC GAC ACC AGC GCA CGA CGG CGC GTC GGT GGT TCC CTC TGT TGC TTT CGC GTC CGG
 ser asp asp thr ser ala gly arg ala val gly val ser leu cys cys phe pro val arg
 123/41 153/51

TTC CGC TTT TTT TCA TCA ACG TTG GAC TGC CGC AGT GGN GAT GTT GGT CGG CGG CDT GTT
 leu ala phe phe ser ser thr leu asp cys arg ser gly asp val gly arg arg arg val
 183/61 213/71

CGG TGC CCT GAC CGG GAT GTT CCT TGG CGC TCG CGG TGC TGC TGG GTT TGC TCA ATG
 arg ser pro asp gly arg asp val pro trp val ser gly cys cys trp val cys ser met
 243/81 273/91

CCC TGC TGG TGC CGC GTT CGG CGG AGT CGA TCA CGG CGA AAG AGC ACC CDT TAA AAC GGT
 pro cys trp cys gly val arg pro ser arg ser pro pro lys ser thr arg CGH ass gly
 303/101 333/111

CGA TGG CGC TCA ACT CGG GAT CGC GAC TGG CGA VTA TGA CGA TGC CTC CGG CGT ATC
 arg trp pro ser thr arg asp trp arg leu ser pro cys leu gly leu ile

SEQ ID N° 17C

FIGURE 17C

partie de la séquence nucléotidique de seq17A

1/1 33/11

ggc tag aac ucc gaa gga gac atc gcg egg ttc agg acc ccg gcc cat cgg atg cgt atc
 gly AMB ass pro glu gly asp leu ala gly arg ccg pro pro ala his arg met arg ile
 61/21 91/31

cgg tcc cgc cgg ttc acc acc gac ata ggg agr ttc ccc tgg ggt gat tcc ggt gog agc
 arg ser arg arg phe thr thr asp ile gly ser tyc pro leu gly asp ser gly ala thr
 121/41 151/51

act gcg ata ugc tcc ggg ggc cod cca tca gtc gat tgg gtt tcc gct gca tcc gac
 thr ala ile arg ser ala gly his arg ser val val asp val val ser ala pro ser ala
 181/61 211/71

cgg aat tca ggt gac gaa gtg agc acc ccc ggg tcc aac ggg ccg ttg gtt tcc tcc tcc
 arg ass CGA gly ala ala val shr shr pro ala gln esp ala pro leu val phe phe ser
 241/71 271/81

gtt gct ttc cgt ccg gtt acc ctt ttt ttc aac aac gtt gga ctg gca gca ggg ggg agt
 val ala phe arg pro val arg leu phe phe ile ass val gly leu ala ala val ale met
 301/101 331/111

tta gtc gca ggc gtt ttc ggt gac acc acc gtt ggg acc atg ttc ttg ggt ctc ggg ctt ggg ctt
 leu val ala gly val phe gly his ile tca val gly met phe leu gly leu gly leu ile
 361/121 391/131

ctg ggt ttc ctc sat gac ctg ctg gtt egg acc ttc acc gag tcc acc acr gca ass gag
 leu gly leu leu ass ala leu leu val arg arg ser ala glu ser ile thr ala lys gln
 421/141 451/151

acc ccc ttc ass cgg tcc atg gac ccc acc tcc gca tcc gag cgg acc acc att acc acc atc
 his pro leu lys atg ser met ala leu ass ala ccc ass arg leu ala ile thr ile
 481/161

ccc ggg ctt atc
 leu gly leu ile

SEQ ID N° 17A*

FIGURE 17A

FEUILLE DE REMPLACEMENT (REGLE 26)

60/185

1/1 31/11
 gct aga acc cag aag gag acc tcc cgg acc tcc gtt gtc ggc acc cgg acc atc gga tgc gta tcc
 ala arg thr pro lys glu thr ser arg val ala gly pro arg pro ile gly cys val ser
 61/21 93/31
 ggt cgc gca gat tca cga cgg acc tcc ggg gct acc ctt tcc gtc att ccc gtc cga cga
 gly arg ala asp ser arg pro thr AMB gly ala thr pro trp val ile pro val arg arg
 123/41 151/51
 ctg cga tac gtc gct cgg egg ggc acc gat cag tcc act egg tgg ttt ccc ccc ctt ccc
 leu arg tyr ala arg arg ala thr asp gln ser ile gly trp phe pro leu his gln pro
 181/61 211/71
 gga att gag gty cgg cgg tgg cgg acc cag ccc aac arg ccc cgt tgg tgg tcc act cgg
 gly ille glu val pro gln OPA arg his gln arg arg the arg arg trp cys phe pro leu
 241/81 271/91
 ttg ctt tcc gtc cgg trc gca ctt ttt tcc tca acc tcc tgg gac cgg cgg cgg tgg cgg tgg
 leu leu ser val arg phe ala phe phe ser ser the leu asp trp pro gln trp arg cys
 301/101 331/111
 tgg tcc cgg ggg bat tcc gtc acc tca cgg tcc ggg tgg tcc tcc tgg gtc tcc tgg tcc
 trp ser pro ala cys ser val OPA arg arg ser gly cys ser trp val ser gly cys
 361/121 391/131
 tgg gtt tgg tca aty ccc tcc egg tcc ggg gtt egg ccc aat cca tcc cgg ccc aag aac
 tcc val cys ser met pro cys trp cys gly val arg pro ser arg ser pro pro lys ser
 423/141 451/151
 acc cgt tcc aac ggt cgg tgg acc tcc acc ccc cat acc gac tgg cgg ccc tcc tcc ccc tcc
 thr arg OCH asn gly arg trp pro ser the arg his arg asp trp arg leu ser pro ser
 483/161
 tcc ggc tgg to
 ser gly OPA

SEQ ID N° 17B'

FIGURE 17B'

1/1 31/11
 ctc gaa ccc tgg aag aga cct tgg ggg tgg acc tcc ggg cca gtc gat ggg ttc ccc
 leu glu pro arg arg arg pro arg gly leu phe ala pro gly pro ser asp ala tyr pro
 61/21 93/31
 gtc gcg ccc att ccc gac cga cat egg gag cta ccc ctt ggg tgg tcc cgg tgg gac gat
 val ala pro ile his asp arg his arg gln leu pro leu gly OPA phe AMB cys asp asp
 123/41 151/51
 tcc gat acc ctc ggc egg cca cgg acc aat ccc tgg ggt ggt tcc ccc tcc acc acc ccc
 cys asp the leu gly gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro
 181/61 211/71
 gag tcc egg tcc egg arg gag gag acc acc gca ggg cat acc gtt ggt tcc ccc tcc tgg
 gln leu arg cys arg ser arg asp asp the ser ala gly arg ala val gly val ser leu cys
 241/81 271/91
 tgg ctt tcc tcc egg tcc cat bat ttt cat ccc ccc tgg act egg ccc arg ggg gat gtt
 cys phe phe ser gly ser pro phe phe his gln arg trp thr gly arg ser gly asp val
 301/101 331/111
 ggt ccc ccc ccc acc ccc tcc bat gag acc acc ggg gat gtt tcc cgg gtt gtt gtt
 gly arg arg arg val arg ser pro arg gly arg asp val leu gly ser arg val ala ala
 361/121 391/131
 ggg ttt ggt cat ccc tgg acc ggt ggt ggg ggg tcc ggg ccc gtc gat ccc ccc ccc agg agg
 gly phe ala gln cys pro ala gly ala ala phe gly AMB val asp his arg gln arg ala
 423/141 451/151
 acc gtt aca aac gtc gat ggc cat tcc ggg acc tcc gag acc ggg gat bat cat cat cat
 pro val lys the val asp ala phe gln lys gly ile ala the gly amp phe his his pro
 483/161
 ccc gtt gat gaa c
 acc ala asp

SEQ ID N° 17C'

61/185

séquence Rv1303 prédicté par Cole et al. (Nature 393:537-544) et contenant partiellement
Seq13A'

1/1 31/11
 atg acg acc cca gtc cag gac gct cgg ttc ggt ttt ccc tct gtt gat ttg cgt ccc gtc gtt
 met thr thr pro sls gln asp als pro leu val phe pro ser val als phe arg pro val
 61/21 31/31
 gtc ctt ttt ttc atc asd gtt ggg ctg gco gca gtg ggc arg ttc gtc gco gyc gtg trc
 arg leu phe phe ile asn val gly leu als als val als met leu val als gly val phe
 123/41 151/51
 ggt sec ctg acg gtc ggg atg ttc ttg ggc ctt ggg tgg ctg ctg ggt ttg ctc asd gcc
 gly his leu thr val gly met phe leu gly leu gly leu leu leu gly leu leu asn als
 181/61 211/71
 ctg ctg gtg cgg cgt tcc ggc gag tgg atc acc gca asa gag ccc ccc tta asa cgg tcc
 leu leu val arg arg ser als glu ser ile thr als als lys glu his pro leu lys arg ser
 241/81 271/91
 atg gco ctc acc tcc gca tcc gca cgg gag att acc acc acc acc ggg ctg atc atc gcc
 met als leu asn ser als ser arg als als ile thr ile leu gly leu ile als als
 301/101 331/111
 tac acc ttc ccc ccc gct gga ttg tcc gtc tgg cgg cgg gac ttc tcc ccc gtc gtc
 tyr ile phe arg phe als gly leu gly val phe gly leu als als phe phe glu val leu
 361/121 391/131
 ctg gtg gca acc arg gco ctg ccc gca ctg asd arg ctg ccc act gog acc gac gac gac
 leu val als thr thr als leu pro val leu lys ius arg thr als thr glu glu pro
 421/141 451/151
 gtc gca act tat tcc tcc asr ggc cag acc ggg gca tcc gac gca arg acc gac gac gac
 val als thr ser ser als gly glu thr gly gly ser gly arg ser als ser asp
 481/161
 gac tga
 asp CFA

SEQ ID N° 17D

FIGURE 17D

Dif d'après Cole et al. (Nature 393:537-544) et contenant Rv1303

1/1 31/11
 tga ggt gcc gca gtg acc acc cca gng oeg gac gcp acc tgg gtc ttt ccc tct gtt gat
 ORF gly als als als val als ths thr pro als glu als pro leu val phe pro ser val als
 61/21 31/31
 tcc cgg ccc gtt oeg cct ttt ttc acc acc gtt ggs ccc gcc gtg gac gtc tgg gtc
 phe arg pro val arg leu phe phe ile als als val als als als met leu val
 123/41 151/51
 gcc ggc gtc tcc ggt ccc phe arg acc gac ggg arg ttc tcc ggt ctc ggg tcc ctg ctg gtc
 als gly val phe gly his leu thr val gly met phe leu gly leu gly leu leu gly
 181/61 211/71
 ttg ctc acc gcc ctg ctg gtc egg cog cog cog cog gac gac tcc acc acc gcc asa gac ccc cog
 leu leu als als leu leu val arg arg ser als glu ser ile thr als lys glu his pro
 241/81 271/91
 cta sac cgg tcc atg gca acc acc acc gca tcc gca tcc gac acc gac acc acc acc acc
 leu lys arg ser als leu asn ser als ser arg leu als ile ile thr ile leu gly
 301/101 331/111
 dtg atc ttc gct taa art tcc cgg uuc gac gac tgg acc egg acc gca acc gca acc
 leu ile als als tyr ile phe arg pro als gly leu gly val val phe gly leu als phe
 361/121 391/131
 ttc cac gng ctg ctg gtc gca acc arg arg gac tcc egg gac ctg acc acc acc acc
 phe glu val leu leu val als thr als leu pro val leu lys iys leu arg thr als
 421/141 451/151
 acc gac gac ccc gca acc acc tat tcc tcc met gpc cag acc egg gca tcc gac gca acc
 thr glu glu phe val als thr tyr ser ser asn gly gln thr gly gly ser gly arg
 481/161
 acc gac gac gac gac tga
 ser als ser asp asp CFA

SEQ ID N° 17F

62/185

31/11

GTC GAA CAG GTA CGG AAG GCG CGG TCG GTC GCT CGG TCC GGT ATC TCG TGT TCA GCC
 val glu gln val arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala
 61/21 31/31

AGC CAG CGG CGG TTA ACG TGG CGG AAC AGG TCG TCT TGG GGT CGG GCA TCA CGG TCG ATG
 ser glu arg pro leu thr trp pro ser arg ser ser trp gly arg ala ser ala ser met
 131/41 151/51

TGG CTC AGG TCG ATA CCC GAG GGG ATG GCA AGT GTC ACC CGG CCA TCC TTC CAC CTC TTT
 try leu arg ser ile pro glu gly met ala ser val thr pro pro ser phe his leu phe
 181/61 211/71

TCA GGT GCA ACG ATG GGG CGA TCG CTG ACG GGG AGC AGA GCC AGC CGC CCC AAC AAG
 ser gly ala thr ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys
 241/81 271/91

ATG CGG AAG RCG ACT CGC CGC CGG ACG CGG CGG AGG CGG CGG AAC CCT AAT CAT
 met arg lys thr thr arg gly pro the pro arg arg pro arg pro asn pro asn his
 301/101 331/111

CAG CGG GTC CGG ATG TTC TCG ACC TAC GGT ATC CGC TCG ACA CTA CTC CGC GTC CTA TCG
 glu pro val pro met phe ser thr tyr gly ile ala ser thr leu leu gly val val leu ser
 351/121

GTC GCC GGG GTC CTC GTC GGT CGG ATG ATC
 val ala ala val val leu gly ala met ile

SEQ ID N° 18A

FIGURE 18A

32/11

TCG AAC AGG TAC CGA AAG CGC CGT CGG TCG CTC GCT CGG CTG GTC TCT CGT GTT CAG CGA
 ser asn ala tyd gly arg arg arg ser leu gly pro leu val ser arg val gln pro
 62/21 62/31

GCC AGC GGC CGT TAA CGT GGC CGA AGA GGT CGT CTT CGG GTC CGG CAT CAG CGT CGA TGT
 ala ser gly arg och arg arg thr gly arg leu gly val gly his gln arg arg cys
 122/41 152/51

GGC TCA GOT CGA TAC CGG AAG GGA TGG CAA GTC TDA CGC CGG CAT CCT TCG ACC TGT TTT
 gly ser gly arg tyr pro arg gly tyd gly val val ser pro arg his pro ser thr ser phe
 182/61 212/71

CGG GTC CAA CGA TCG CGC CAT GUC TGA CGG CGA GAG CGA CGG CGC ACC GGC CGA AGA AGA
 arg val gln arg ser gly his ala CGA arg gly ile glu pro ala thr gly pro arg arg
 242/81 272/91

TGG CGA AGA CGA CTC CGG CGC CGA CGG CGG CGA CGG CGC CGG CGC CGA ACC CGA ATC ATC
 cys gly arg arg leu ala ala ala arg arg arg gly gly arg arg arg arg arg thr gln ile ile
 302/101 332/111

AAC CGG TCG CGA TGT TCT CGA CCT ACC GTC TCG CCT CGA CGC TAC TCG CGG TGC TAT CGG
 ser arg ser arg cys ser arg pro thr val ser pro arg his tyr ser ala cys Tyr arg
 362/121

TCG CGG CGG TGG TCG TGG GTC CGA TGA TC
 ser pro arg ser cys trp val arg GPR

SEQ ID N° 18B

FIGURE 18B

FEUILLE DE REMPLACEMENT (REGLE 26)

63/185

3/1 33/11
 CGA ACA GGT ACC GAA GGC GCC GTC GGT CGC TCG GTC CGG TGG TAT CTC GTC GTC TTC AGC CAG
 arg thr gly thr glu gly ala val gly arg ser val arg trp tyr leu val phe ser gin
 63/21 53/31
 CGG GCG CCC GTT AAC GTG GCC GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG
 pco ala ala val asn val ala glu val val val leu gly ser gly ile ser val asp val
 123/41 153/51
 GCT CAG GTC GAT Acc CGA GGG GAT GGG AAG GGT CAG CGG GGC ATC CTT CCA CCT CTT TTC
 ala glu val asp thr arg gly asp gly lys cys His pro ala ile leu pro pro leu phe
 183/61 213/71
 GGG TGC AAC GAT CGG CCC ATG CCT GAC GGG GAG CAG AGC CAG CGG CAA GAA GAT
 gly cys asn asp arg ala met pro asp gly glu din ser gin pro pro ala gln glu asp
 243/81 273/91
 GCG GAA GAC GAC TCG CGG CCC GAC GGC GCG GAC GGC GCG GAA CCC AAA TCA TCA
 ala glu asp asp ser arg pro asp ala ala ala ala ala glu pro lys ser ser
 303/101 333/111
 GCC GGT CCC GAT GTT CTC GAC CTA CGG TAT CGC CTC GAC ACT ACT CGG CGT GCT ATC CGT
 ala gly phe asp val leu asp leu arg tyr arg leu asp thr thr arg arg ala ile gly
 363/121
 CGC CGC GGT CGT GCT CGG TCC GAT GAT C
 arg arg gly ala gly cys asp asp

SEQ ID N° 18C

FIGURE 18C

partie de la séquence nucléotidique de seqIDN

1/1 31/11
 GAA GGC GCG GTC GGT CGG CGC TCG GTC CTC GTC GTC TTC AGC CAG CGA GCG GCG GCT
 glu gly ala val gly arg ser val arg trp tyr leu val phe ser gin pro ala ala val
 61/21 61/31
 AAC GTG GCG GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG GCT CAG GTC GAT
 asn val ala glu gin val val leu gly ser gly ile ser val asp val ala gin val asp
 121/41 151/51
 ACC CGA GGC GGC ARG TGT CAC CGC GCG ATC CCT CCA CCT CTT TTC GGG TGC AAC GAT
 thr arg gly asp gly lys cys His pro ala ile leu pro pro leu phe gly cys asn asp
 181/61 211/71
 CGG GCC ATG CCT GAC GGG GAG CAG AGC CAG CGG CGC CAA GAA GAT GCG GAA GAC GAC
 arg ala met pro asp gly glu ser gin pro ala gin pro asp ala glu asp ala glu asp asp
 241/81 271/91
 TCG CGG CCT GAC GGC GGG GAG CGC GCG GCG GCA GAA CCC AAA TCA TCA GGC GGT CGG ATG
 ser arg pro asp ala ala ala ala ala ala ala glu pro lys ser ser ala ala ala pro met
 301/101 331/111
 TTG TCG ACC TAC GGT ATG GCG TCG ACA CTA CTG GCG GTC CTA TCG GTC GCG GCG GTC GTC
 phe ser thr tyr gly ala ala ser thr leu leu gly val leu ser val ala ala val val
 361/121
 CTG GGT GCG ATG ATC
 leu gly ala met ala

SEQ ID N° 18A'

FIGURE 18A'

FEUILLE DE REMPLACEMENT (REGLE 26)

64/185

1/1 31/11
 CGG AAG GCG CGG TCG GTC GCT CGG CCT GOT ATC TCG TGT TCA CGG AGC CGG CGG
 arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala ser gln arg pro
 61/21 91/81
 TTA ACG TGG CGG AAC AGG TCG TGT TCG GGT CGG GCA TCA CGG TCG ATG TGG CTC AGG TCG
 leu thr trp pro asn arg ser ser trp gly arg ala ser ala ser ser met trp leu arg ser
 121/41 151/51
 ATA CCC GAG GGG ATG GCA ACT GTC ACC CGG CCA TCC TTC AAC CGG TTT TCG GGT GCA AGC
 ile pro giv gly met ala ser val thr pro pro ser phe his leu phe ser gly ala thr
 181/61 211/71
 ATC GGG CCA TGC CTG ACG GGG AGC AGA CGC AGC CGC AAC AAG AAG ATG CGG AAG AGC
 ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys met arg lys thr
 241/81 271/91
 ACT CGG CGC CGG ACG CGG CGG AGG CGG CGG CGG AAC CCA ATT CAT CAG CGG GTC CGA
 thre arg gly pro thr pro arg arg pro pro ser phe his gln pro val arg
 301/101 331/111
 TGT TCT CGA CCT AGG GTA TCG CCT CCA CAC TAC TCG GGC TGC TAT CGG TCG CGG CGG TCG
 cys ser arg pro thr val ser pro arg his tyr ser ala cys tyr arg ser pro arg ser
 361/121
 TGC TGG GTG CGA TGA TC
 cys trp val arg OPA

SEQ ID N° 18B'

FIGURE 18B'

1/1 31/11
 GGA AGG CGG CGT CGG CTC GOT CGG CTC GTC TGT CGT GTC CAG CGA CGC AGC CGG CGT
 gly arg arg arg arg ser leu gly pro leu val ser arg val gln pro ala ser gly arg
 61/21 91/81
 TAA CGT GGC CGA ACA GGT CGT CTT CGG GTC CGG CAT CAS CGT CGA TGT CGC TCA GGT CGA
 CGA arg gly arg thr gly arg leu gly val gly his gln arg arg cys gly ser gly arg
 121/41 151/51
 TAC CGG AGG GGA TGG CAA GTG TCA CGG CGT CAT CCT TCG ACC TCT TTT CGG GTC CGA CGA
 tyr pro arg gly arg gln val ser pro arg his pro ser thr ser phe arg val gln arg
 181/61 211/71
 TCG GGC CAT CGC CGG CGA GAG CGA GAG CGC ACC CGG CGA AGA AGA TGG CGA AGA CGA
 ser gly his ala CGA arg gly ala gln pre ala thr gly pro arg arg cys gly arg arg
 241/81 271/91
 CTC CGG CGC CGA CGG CGC CGG CGG CGC CGA AGC CGA ATT ATC AGG CGG TCG CGT
 leu ala ala arg arg arg gly arg arg arg gly arg the gln lle ile ser arg ser asp
 301/101 331/111
 GTT CTC GAC CGA CGG TAT CGG CGC AGC ACT ACT CGG CGT CGT ATC CGT CGC CGC CGT CGT
 val leu asp leu arg arg myr arg leu asp the thr arg arg ala lla gln arg arg gly arg
 361/121
 CGT CGG TGG GAT GAT C
 ala gly cys asp asp

SEQ ID N° 18C'

FIGURE 18C'

FEUILLE DE REMPLACEMENT (REGLE 26)

65/185

séquence PvC199 prédictée par Cole et al. (Nature 333:537-544) et contenant seq18A'

1/1	31/11
atg cct gag ggg gag cag aca ccc ggc cca gaa gat gng gaa gac gac tcc egg	
Met pro asp gly glu gln ser gln pro pro ala gln glu asp ala glu asp asp ser arg	
61/21	31/31
ccc gsc gcc gcg gag gcc gcc ggg gcc gaa gca tca gcc ggt ccc arg ttc tcc	
pro asp ala ala glu ala ala ala glu pro lys ser ser ala gly pro met phe ser	
121/41	31/51
acc tac ggt atc gcc tcc tca cta ctc ggc gtg cta tcc gtc gcc ggg gtc gtg ctg ggt	
thr tyr gly ile ala ser thr leu leu gly val leu ser val ala ala val val leu gly	
181/61	211/71
gog atg atc tgg tcc gca csc ccc gat gac tcc ggc gag cgt acc tac ctg acc cgg gtc	
ala met ile trp ser ala his arg asp ser gly glu arg thr tyr leu thr arg val	
241/81	231/91
atg ctg acc gcc gct gaa tgg acg gcc gtg ctg atc acc atg acc gco gac acc atc gat	
met leu thr ala ala glu trp thr ala val ala ASN met ASN ala ASP ASN ile ASP	
301/101	331/111
gcc agn ctc cag cga ctg cac gac gga acg gtc ggt ccc acc acc gac ttc gac gtc	
ala ser leu gln arg leu his asp gly thr val gly gla leu ASN thr ASP phe ASP ala	
361/121	231/131
gtc gtg cag ccc tac ccc cag gng gtg gac acg tcc ccc acc agc acg agc ggc agg atc	
val val gln pro lys arg gln val val gln lys leu arg thr his ser ser gly arg ile	
421/141	451/151
gag gcg gta ggc atd gat atg gtg cac ccc gag ctg gat acc cag tcc ggt gac gac gca	
glu ala val ala ile asp thr val his arg glu leu ASP thr gln ser gly ala ala arg	
481/161	511/171
ccc gts gta acc acc acc amt ttg cca ccc ttt gco act egg acc acc gac tcc gty ccc ctg gtc	
pro val val thr thr lys leu pro pro phe ala ala arg thr ASP ser val leu leu val	
541/181	571/191
gag acg ttt gtc agt ggg acc gco ggc amt ccc cag acc gtc cac tgg acc ttt cgg	
ala thr ser val ser gln ASN ala gly ala lys pro gln thr val his trp ASN leu arg	
601/201	631/211
ctc gat gtc tcc gat gng gac ggt acg atc tcc cgg ttt ggg tgg tcc att cca tga	
leu asp val ser asp val asp gly lys leu met ile ser arg leu glu ser ile arg GAA	

SEQ ID N° 18D

FIGURE 18D

66/185

ORP à l'après Cole et al., (Nature 393: 537-538).

I/1
tac tcc gat gac gga ttg ggt gaa atg cat cat gta acg egt cgg gtc ctt gga att ggt
GCH ser asp ala gly leu gly glu met his gln val thr gly arg val phe gly ile gly
61/731
atc gac ata gac tcc gat gco gco gct acg gac ggc acc ttc cag agt gco aag gyc gac
iles asp ile asp ser asp ala als ala his ala gly thr leu gln ser ala lys gly gly
123/41
ggc cca ttc egt ggc gtc ggt gct gtc eat cgt ggc cca ttc gtc gtc gtc cag egg rtg
gly gln phe gly gln val gyl arg ala val asp ala arg gyl gln phe val val gln arg leu
181/41
cat acc tcc pcc ctc gac gac ggc ttc ctc gtc gag gac gca gct ggc gtc gta gco gat ggc
his pro cys ala leu asp gly phe leu gln ala glu gln ala gly val gln val ala asp ala
241/81
771/91
ctg cgc atc gtc gtc gtc tcc atc gtc ttc gtc
leu arg ile gly ala tyr arg ser thr cys lys ala gly leu asp asp gln val ser his
302/101
tgc tgc tcc ggc gyc gtc gaa cag gct acg gac ggc acc gac gtc gtc gtc ctc tcc tcc
tcc cys leu gly ala val gln gln ala thr glu gly ala val gln arg ser val arg trp
361/121
tar ccc gtc ttc acc ctc ccc gca
tgt gtc
tgt cys leu gly ala val gln gln ala thr glu gly ala val gln arg ser val arg trp
391/131
tar ccc gtc ttc acc ctc ccc gca
tgt gtc
tgt cys leu val phe ser gln pro ala ala val asp ala val asp ala gln val gln val gln ser
421/141
ggd acc acc gtc val gtc act ctc gtc
gly ile ser val asp val ala gln val asp thr arg gly arg gln lys cys his pro ala
441/161
att ctt cca acc ctt ttc ggg tcc acc acc gat cgg gcc atg ctc gac ggg gag gag egg acc gag
ile leu pro pro leu phe gly cys asp asp arg ala met pro asp gly gln gln ser gln
541/181
ccc ccc gcc cca gca gca gat gcc gac gac gac gad tag cgg acc gac gca gcc gac gcc
pro pro ala gln gln asp ala gln asp asp ser arg pro asp ala ala gln ala ala
601/201
gcc gca ccc aca tca tca gca gca ggt acc atg acc tag ccc tag acc tcc gtc acc ctc
ala gln pro lys ser ser ala gly pro ser phe ser thr tyr gly ile ala ser ser thr leu
661/221
ctc gac gtc cta tag gtc gca gcy gtc
gln gly val leu val ala ala val val val gln gln val gln val gln val gln val gln
721/241
gtc gac tcc gtc
asp asp ser gly gln arg arg trp tyr leu thr arg val met his ala ala gln gln trp thr
781/261
gtc gtc gtc ctc atc acc atc gtc gac acc atc gtc gtc gtc gtc gtc gtc gtc gtc
val gln lys ser gln
841/281
ggg acc gtc gtc gtc ccc acc acc gac tac gtc gtc gtc gtc gtc gtc gtc gtc gtc
gly thr val gln gln leu asp thr asp phe gln gln val val gln pro tyr arg gln val
901/301
gtc gag acc ttg ccc acc
val gln lys ser gln
961/321
acc acc gac ccc gat acc acc acc acc ggc gca
his arg gln leu asp thr gln ser gln
1021/341
ccg ttg gtc act tcc acc acc acc ttg gtc ctc
pro phe ala thr arg thr asp ser val leu
lys val ala ser ser val val val val val val
1081/361
ggc gcc aas acc acc acc acc gtc acc acc acc
gln
1141/381
acc acc acc acc acc acc acc acc acc
lys leu met lle ser and leu gln ala lle
lys val asp val asp val asp val asp val
1201/401

SEQ ID No: 36

FIGURE 187

FEUILLE DE REMPLACEMENT (RÈGLE 26)

67/185

31/11
 GTT CGG CAA CGG GGT GAG GRC CGA CGC GAT GAT GGC GCA ACT ATC GAA ACT GCA GGA CAT
 val ala gln arg gly gln his arg arg asp asp gly ala thr ala glu thr ala gly his
 61/21 91/31
 CGC CAA CGC CAA CGG CGC CGC TCG CCC GGT GGG CAC CCC TGG CTA TCA GGC GAG CCT CGA
 arg gln arg gln arg arg his ser arg gly gln his pro trp leu ser gly gln arg arg
 121/41 151/51
 CTA TGT GGT AAA CAC ACT CGG CAA CAG CGG TTT TGA TGT GCA AAC CCC GGA GTT CTC CGG
 leu cys gly lys his rhr ala gln gln arg phe GPR cys ala ser pro gly val leu arg
 181/61 211/71
 TCG CGT GTT CAA GGC CGA AAA AGG GGT GAC CCT CGG CGG CAA CAC CGT GSA GGC GAG
 ser arg val gln gly arg lys arg gly gly asp pro arg arg gln his arg gly gly glu
 241/81 271/91
 GGC GCT CGA GTA CAG CCT CGG CGC ACC GGC GGA CGG GGT GAC CGG CCC GCT GGT GGT GGC TCG
 gly ala arg val gln pro arg his thr ala gly ser gly asp gly pro ala gly gly cys
 301/101 331/111
 CGC CGG CGA CGA CAG TCG GGG CTG CAS TCC CTC GCA CTA CGA CAG CCT GGC GGT GTC CGG
 pro arg arg arg gln ser gly leu gln ser val gly leu arg gln ala als gly val arg
 361/121
 TGC GGT GGT GGT AGA TC
 cys gly gly als gly arg

SEQ ID N° 19A

FIGURE 19A

22/11
 TTG CGG AAC CGG GTC AGG ACC GAC CGG ATG ATG CGG CAA CTA TGG AAA CTG CGG GAC ATG
 leu arg asn gly val ser thr asp ala met met ala gln leu ser lys leu gln asp ala
 62/21 93/31
 GGC AAC CGG AAC GAC GAG ACT CGG GCG GTC GGC ACT CCT GGT TAT CAG GGC AAC GTC GAC
 ala ser ala asn asp gly thr arg ala val gly the pro gly tyr gln ala ser val asp
 122/41 152/51
 TAT GTG GTA AAC ACA CTG CGC AAC AGG TTT GAT GTG CAA AAC CCT CGG TTC TCG GCT
 tyr val val asn thr leu arg asn ser gly phe asp val val thr pro gln phe ser ala
 182/61 212/71
 CGC GTC TTC AAG GCG GAA AAC CGG CTG GTC AAC CTC CGC CGC AAC AAC GTG GAG GCG AGG
 arg val phe lys ala gln lys gly val val thr leu gly gly asn thr val gln ala arg
 242/81 272/91
 GCG CTC GAG TAC AGC CTC CGC ACA CGG CGC GAC GGG CTG AGG GGC CGG CTG GTC GCT GCG
 ala leu gln tyr ser ala gln thr pro phe asp gly val thr gly pro leu val ala als
 302/101 332/111
 CGG CGC GAG AGT CGG CGG TGC AGT CGG TCG GAC TAG GAG AGG CTG CGG GTC TCG GGT
 pro als asp asp ser phe gly cys ser pro ser asp tyros asp arg leu phe val ser gly
 362/121
 GCG GTC GIG CTG GTA GAT C
 als val val leu val asp

SEQ ID N° 19B

FIGURE 19B

68/185

33/11

TGC GCA ACG GGG TGA GCA CGG ACG CGA TGA TCG CSC AAC TAT GCA AAC TGC AGG ACA TCG
 cys ala thr gly GPA ala pro thr arg GPR trp arg ASN tyR arg ASN cys ala THR ser
 63/21 93/31

CCA ACG CCA ACG ACG GCA CTC CGG CGG TGG GCA CGC CTG GCT ATC AGG CCA CGG TCG ACT
 pro THR pro THR ala Ile ala arg TRP ala pro LEU ala Ile ARG pro ALA ser THR
 123/41 153/51

ATG TGG TAA ACA CAC TGC GCA ACA CGC GTT TGG ATG TGC AAA CCC CGG AGT TCT CCG CTC
 met TRP OCH THR HIS CYS ALA THR VAL ILE MET CYS LYS PRO ARG SER SER PRO LEU
 183/61 213/71

GCG TGT TCA AGG CGG AAA AAG GCG TGG TGA CCC TCG CGG GCA ACA CGC TGG AGG CGA CGG
 ala CYS SER ARG PRO LYS LYS GLY TRP GPR SER ALA ALA THR PRO TRP ARG ARG GLY
 243/81 273/91

CGG TGG AGT ACA CGC TCG GCA CGAC CGG CGG TGA CGG CGC CGG TGG TGG CTG CCT
 ARG SER SER THR ALA ALA HIS ARG ARG GLY GPR ARG ALA ARG TRP TRP ILE PRO
 303/101 333/111

CGG CGG AGC ACA GTC CGG CCT GCA GTC CGT CGG ACT AGC ACR CGC TGC CGG TGT CGG GRS
 PRO PRO THR THR VAL ARG ALA ALA VAL ARG ARG THR THR GLY GLY ARG CYS PRO VAL
 363/121

CGG TGG TGC TGG TAG ATC
 ARG TRP CYS TRP AMB ALA

SEQ ID N° 19C

FIGURE 19C

partie de la séquence nucléotidique de SeqIDN°A

1/1

31/11

CTA TCG AAA CTG CAG GAC ATC CGC AAC AAC GAC GGC ACT CGC CGG GTC CGC AGC CCT
 Ile ser Lys Ile Glu Asp Ile Ala Asn Ala ASN ASN ASP GLY THR ARG ALA VAL GLY THR PRO
 61/21 91/31

GGC TAT CAG CGC AGC GTC GAC TAT GTG GTC AAC ACA CGT CGC CGC AAC AGC AGC GGT TTT GAT GTC
 GLY TYR GLN ALA SER VAL ASP TYR VAL VAL ASN THR ILE ARG ASN ASN GLY PHE ASP VAL
 121/41 151/51

CAA ACC CGG SAG TTC TCC OCT CGC GTC TTC AAG GCC GAA AAA CGG GTC GTC ACC CGC CGC
 GLN THR PRO GLU PHE SER ALA ARG VAL PHE GLN GLU GLY GLY VAL VAL THR ILE GLY
 181/61 211/71

GCG AAC ACC GTC SAG CGG AGG CGG CTC GAG TMC AGC CTC CGC ACA CGC CGC GAC CGG GTC
 GLY ASN THR VAL GLN ALA ARG ALA LEU GLU TYR SER GLY THR PRO PRO ASP GLY VAL
 241/81 271/91

AGC GCG CGG CTG CTG GCT CGC CGC GAC GAC AGT CGG GGC TWT AST CGG TCG GAC TAC
 THR GLY PRO LEU VAL ALA ALA ALA PRO ALA ASP ASP SER PRO GLY GLY ASN ASN PRO SER ASP GLY
 301/101 331/111

GAC AAG CTG CGG GTG TCC GGT CGC GTG GTG CTG GTA GAT C
 ASP ARG LEU PRO VAL SER GLY ALA VAL VAL LEU VAL VAL ASP

SEQ ID N° 19A'

FIGURE 19A

69 / 185

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1/1 31/11
TAT CGA AAC TGC AGG ACA TCG CCA AGC CCA ACG AGG GCA CTC GCG CGG TGG GCA CCC CTG
tyr arg asn cys arg thr ser pro thr pro thr ala leu ala arg trp ala pro leu
61/21 91/31
GCT ATC AGG CCA CGG TGG ACT ATG TGG TAA ACA CAC TGC GCA ACA GCG GTT TTG ATG TGG
ala ile arg pro ala ser thr met trp CTC his cys ala thr ala val leu met cys
121/41 151/51
AAA CCC CGG AGT TCT CGG CTC GCG TGT TCA AGG CGG AAA AAG GGG TGG TGA CCC TGG CGG
lys pro arg ser ser pro leu ala cys ser arg pro lys lys gly trp DPA pro ser ala
181/61 211/71
GCA ACA CGG TGG AGG CGA CGG CGG TGG ATG AGT ACA GCG TGG GCA CAC CCC CGG AGC GGG TGA
ala thr pro trp arg arg gly arg set ser thr ala ser ala his arg arg arg the gly DPA
241/81 271/91
CGG GGC CGC TGG TGG CTG CGG CGG CGG AGC AGC GTC CGG CCT GCA GTC CGT CGG ACT AGC
arg ala arg trp trp leu pro pro pro the val arg ala ala val arg arg thr thr
301/101 331/111
ACA GGC TGC CGG TGT CGG GTC CGG TGG TGC TGG TAG ATC
thr gly cys arg cys pro val arg trp cys trp ANB ile

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SECO ID N° 19B*

FIGURE 19A*

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1/1          31/11
ATC GAA ACT GCA GGA CAT CGC CAA CGG CGG CAC TGG CCC GST GGG CAU CCC TGG
his gly the his gly his arg gln arg gln arg gln arg his ser arg gly gly his phe trp
61/21          91/31
CTA TCA GGC CAG CCT CGA CTA TGT AAA CAT ACT CGG CAA CAG CGG TTT TGA TGT GCA
leu ser gly gln arg arg leu cys gly lys his thr ala gln gln arg phe GKA cys ala
121/41          151/51
AAC CCC GGA GTT CTC CGC TCG CCT GTT CAA GGC CGA AAA AGG GGT GGT GAC CCT CGG CGG
asn pro gly val leu arg ser arg val gln arg lys arg gly gly gln asp pro arg arg
191/61          211/71
CAA CAC CGT CGA GGC GAG GGC CCT CCA STA CAG CCT CGG CGC ACC CCC GGA CGG GGT GAC
gln his arg gly gly glu gln gln arg val gln pro arg his thr ala gly arg gly asp
241/81          271/91
GGG CGC GGT GGT GGC TGC CCC CGC CGA CGA CAG TCC GGG TTC CAG TCC GTC CGA CTA CGA
gly pro ala gly gly cys pro arg arg arg gln ser gly Leu gln ser val gly leu arg
301/101          331/111
CAG CCT GGC GGT GTC CGG TGC GGT GGT GGT GGT AGA TC
gin ala ala gly val arg cys gly gly ala gly arg

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SEQ ID N° 19C5

FIGURE 39C'

70/185

sequence Rv041B prédicté par Cole et al. (Nature 393;537-544) et correspondant
seg1SA'

1/1 31/11
 atg gtg aac aaa tcc agg atg atg ccc ggg gtc ctg gcc gtg gct gtg gtc gtc gca tic
 Met val asn lys ser arg met met pro ala val leu ala val ala val val ala phe
 61/21 91/31
 ctg acc acc ggc tgt atc cgg tgg tct acc cgg cgg ccc gtt gtt acc ggc tcc gct
 leu thr thr gly cys ile arg trp ser thr gln ser arg pro val val val asn gly pro ala
 121/41 151/51
 gcc gca gag ttc gac gtt ggg ttc agg aac cgg gtc agg acc gac gcg atg atg gcg ccc
 ala ala glu phe ala val ala leu arg asn arg val ser thr asp ala met met ala his
 181/61 211/71
 ctc tgg aac tgg ccc gac atc gcc aac gac gac gcu act ccc gcc gtc agg agg acc ccc
 leu ser lya leu gln asp ile ala asn asp gly thr arg ala val gly thr pro
 241/81 271/91
 ggc tat acc gcu agg gtc gac tat gtg gta aac acc ccc ccc acc agg ggt ttt gac gtc
 gly tyr gln ala ser val asp tyr val val asn thr leu arg asn ser gly phe asp val
 301/101 331/111
 ccc acc ccc gag ttc tcc gct agg cgt gtc ttc asp gcc gaa gaa ggg gtc agg acc ccc gcc
 gln thr pro glu phe ser ala arg val phe ala gln ala lys gly val val thr leu gly
 361/121 391/131
 ggc acc acc gtc gag ccc agg ccc gtc agg tac agg ccc gcc aac agg ccc gag ggg gtc
 gly asn thr val gln ala arg ala leu gln tyr ser leu gly thr pro pro asp gly val
 421/141 451/151
 aeg ggc ccc ctg gtc
 thr gly pro leu val ala ala pro ala asp asp ser pro gly cys ser pro ser gac tyr
 481/161 511/171
 gag agg ctg ccc gtc gtc tcc ggt ggg gtc
 asp arg leu pro val ser gly ala val val leu val asp arg gly val cys pro phe ala
 541/181 571/191
 cag gag gaa gca gca gcc gcc gcc ccc gag ccc gtc gtc gtc gtc gtc gtc gtc gtc
 gln lys gln asp ala ala ala gln arg gly ala val ala leu ile ile als asp asn ile
 601/201 631/211
 gag gag ccc atg ggc acc ccc ggg gct ass acc gac gtc agg atp org gtc gtc
 asp glu gln ala met gly thr leu gly ala ass thr asp val lys ile pro val val
 681/221 691/231
 aeg gtc acc aag tcc gtc gga ttc ccc
 ser val thr lys ser val gly phe gln leu arg gly gln ser gly pro thr thr val lys
 721/241 751/251
 ctc acc gcc ggc acc ccc agt ttc aag gac gtc acc gtc atc gcc aag aag aag acc ggg
 leu thr ala ser thr gln ser phe lys ala ala arg val ile ala gln thr lys thr gly
 781/261 811/271
 tcc tcc gcc acc gtc
 ser ser ala asn val val met ala gly ala his leu asp ser val pro gly val pro gly
 841/281 871/291
 atc acc gac acc ggc tcc gga gtc
 ile asn asp asn gly ser gly val ala ala val leu gln thr ala val gln his gly asn
 901/301 931/311
 tcc acc cat gtc tcc acc gcc gta ccc gtc gtc tcc tcc tcc ggc gtc gtc gtc gtc gtc
 ser pro His val ser asn ala val arg phe ala phe trp gly ala gln gln phe gly leu
 961/321 991/331
 att ggc tcc ccc aac tac tcc gtc gac tcc gtc gac atc gac gac gtc acc gcc acc gcc ctc
 ile gly ser arg asn cys val gln ser leu asp ile asp ala leu lys gly ile ala ile leu

SEQ ID N° 19 D

FIGURE 19D

FEUILLE DE REMplacement (REGLE 26)

71/185

1021/341 1031/351
 tat csg acc ttc gac atg ttg ccc tcc cog acc ccc ggt tac ttc acc tac gag ggt gag
 tyr leu asn phe asp met leu ala ser pro asn pro gly tyr phe thr rys esp gly asp
 1031/361 1111/371
 csg ttg ctc cog cta gag gac ggc ccc ggt cag cgg gtc gaa ggc tcc gag ggt acc
 glu ser leu pro leu asp ala arg gly gln pro val val pro glu gly ser ala gly ile
 1141/381 1171/391
 gag cgc acc ttc gtc gcc tat ctg atg gag gac gag acc ccc gag gag acc tcc ttc
 glu arg thr phe val ala tyr leu lys met ala gly lys thr ala gln asp thr ser phe
 1201/401 1231/411
 gag ggt cgg tcc gac tac gag ggc ttc acc ccc gag acc ccc tcc ggt ggc ctg ttc
 asp gly arg ser asp tyr asp gly phe thr leu ala gly ile pro ser gly gly leu phe
 1261/421 1291/431
 tcc ggc gct gag gtc gag gag acc tcc gca gag ctc tgg ggc gyc acc gco gag
 ser gly ala glu val lys lys ser ala glu gln ala glu leu trp gly gly thr ala asp
 1321/441 1351/451
 gag cct ttc gag ccc acc tat cac gag asq acc gag acc ctg gag cat acc gag ccc acc
 glu pro phe asp pro asn tyr his gln lys thr asp thr leu asp his ile asp arg thr
 1381/461 1411/471
 gcg ctc ggt ats acc ggd gct ggc gtc gcy tac gca ggt ggt tcc tat gca cgg gag ctc
 ala leu gly ile ASN gly ala gly Val ala Tyr ala Val gly Ile Tyr ala Gln Asp Leu
 1441/481 1471/491
 ggc gyc acc acc ggg gtt cog gag atg gcy gag gag ccc acc ccc ctc att gca acc acc ccc
 gly gly pro asn gly Val pro Val met ala Asp Arg Thr Arg His Ile Ile ala Lys Pro
 1501/501
 tga
 OPA

SEQ ID N° 19D (suite)

FIGURE 19D (suite)

72/185

ORS d'après Cole et al. (Nature 1961;537-540) et contenant aussi

31/11
tag gcc att cca cgg rct gtt cgt tgg acc ggt cgg tag gat gcg sas got gec cgg cgg
AMB ala ile gin arg ser val arg leu ile gln arg trp asp ala lys ala ala arg arg
61/21 91/31
cag ggc cgg tct aet ctg ggc gcg atg gtc acc aac tcc egg atg atg cgg pgg gty cgg
gin ala arg acr ser ASN leu gly ala met val ass lys ser arg met met pro ala val leu
121/41 151/51
gcc gtg gct gtc gtc gca ttc ctg acc aeg ggg tgg atc cgg tgg tct aeg cgg tag tgg
ala val ala val val ala pho leu thr the gly cys ile gln asp trp ser thr gin ser
181/61 211/71
cgg ccc gtt gtt aac pgg ccc get gec gca tgg ttc gec gtt pgg tgg cgg ccc sas cgg gtg
arg pro val val ass gly pro ala ala ala glc phe ala val ala leu arg ass arg val
141/81 271/91
agg ecc gac gcg atg atg ggg cac cta tgg aas cgg cag gac atc gec ass gct ass gag
ser thr asp ala met met ala his leu ser lys leu gin asp ile ala ass ala ass ass asp
191/101 331/111
ggg act cgg ccc gtt gtc gec acc ccc ggc sat agg ggg age gec gac tat gtc gtc ass ecc
gly thr arg ala val gly thr pro gly tyr gin ala ser val asp tyr val val val ass thr
361/121 391/131
ctg cgg sac aco ggg rtt gat gtc sas acc cgg gag ttc tcc gct cgu gng ttc aag gag
leu arg ass set gly phe asp val gin thr pro glu phe ser ala arg val phe lys ala
421/141 451/151
gaa ass ggg gtc gtc acc ctc egg ggg sac acc atg gag gag ggg egg ggg stc gag tac aco
glu lys gly val val thr leu gly gly ass the val glu ala arg ala leu glu tyr ser
481/161 511/171
ctc ggg sea ccc ccc gag egg gtc acc ggc ccc ctg atg gct gec ccc ggg gac gac agt
leu gly thr pro pro asp sly val thr gly pro leu val ala ala pro ala asp asp ser
661/181 571/191
ccg ggg tgg agt ccc tgg gac tac gag acc ctg ccc atg tcc ggt ggg gtc gtt gtc gta
pro gly cys sea pro ser asp tyr ass arg leu pro val ser gly ala val val leu val
661/201 631/211
aat cgg ggc gtc tgg cat ttt gec cag cag gaa gag gca ggg gca ggg ccc ggg ggg ggg
asp arg gly val cys pro phe ala glu lys glu arg ala ala ala gin arg gly ala val
661/221 591/231
ggc ctg atc stt got gac sac acc ctc gag gag gag pgg atc egg ggg acc rtg ggg gec ass
ala leu ile ala ass asp ass ile asp glu gin ala met gly gly thr leu gly ala ass
721/241 751/251
acc gac gca bac stc ccc gtc gtc gtc agt gtc acc aac tgg gtc gga ttt cag cta ccc ggs
thr asp val lys ile pro val val ser val thr lys ser val gly phe gin leu arg gly
781/261 811/271
cag tcc ggg cda acc acc gtc aag ctc aag ggg acc acc tgg gtc gga ttt cag cta ccc ggs
gin ser gly pro thr thr val lys leu thr ala ser the gin ser phe lys ala arg ass
841/281 871/291
gtc aac gcp cag acc aag aag ggg tgg tgg gtc acc ggg acc acc tgg gtc gca tgg ggg gac kty
val ile ala gin thr lys thr gly ser set ala ass val val met ala gly ala his leu
901/301 931/311
gac acc gtt ccc gaa gga ccc ggg stc acc gac acc ggg tgg ggg gtc acc ggg gtc gtc
asp ser val pro glu gly pro gly ile ala asp ser gly ser gly val ala ala val leu
961/321 991/331
giv acc gca ctt ggg ctt ggg ass tcc cgg acc gtc tgg tgg gtc gca tgg ggg gac kty
thr ala val ala leu gly ass ser pro his val ser gca ala val val who ala ala

550 30 N° 36 5

FIGURE 19F
FEUILLE DE REMPLACEMENT (RÈGLE 26)

73/185

1021/341 1051/351
tgg ggc gac gag gaa ttc ggn ctg att ggg rna cga sac tsc gtc gac tcc gtc gac acc
ttc gly ala glu glu phe gly leu ile gly ser arg acc tyr val glu ser leu asp ile
1081/361 1111/371
gac ggc ttc ssa ggc acc tcc gcg ctg cat tcc gac atg ttg gcy tcc tcc cgg acc cag
asp ala leu lys gly ile ala leu tyr leu ass phe asp met leu ala ser pro ass pro
1141/381 1171/391
ggk tac ttc acc tcc gac ggc gac cag tog ctg ccc cta gac gcc cgc ggt cag cgg cgt
gly tyr phe thr tyr asp gly asp gin ser lsc pro leu asp ala arg gly gin pro val
1201/401 1231/411
gtg ccc gaa ggc tcc ggc ggt atc gag ccc acc tcc gtc gac tat ctg ccc atg gcc ggc
val pro glu gly ser ala gly ile glu arg thr phe val ala tyr ile lys met ala gly
1261/421 1291/431
aaa acc ggc cag gac acc tcc ttc gac ggt acc tcc gac tcc gac ggc ttc acc ccc gcc
lys thr ala gln asp thr ser phe asp gly acc ser asp tyr asp gly phe thr leu ala
1321/441 1351/451
ggc acc ccc tcc ggt ggc ctg tcc tcc ggc gtt acc gtc acc asp tcc gcc gag caa gcc
gly ile pco ser gly gly leu phe ser gly ala glu val lys ser ala glu gln ala
1361/461 1411/471
gag ctc tgg ggc ggc acc gcc gac gac acc tcc gat acc acc tat ccc cag acc acc gac
glu leu trp gly gly thr ala asp glu pro phe asp asp met tyr his gln lys thr asp
1441/481 1471/491
acc ccc gac cat acc gac ccc acc ggc acc tcc ggt acc acc ggc gct ggc gtc gcc gac tat ggc
thr leu asp his ile asp arg thr ala leu gly ile ass gly ala gly val ala tyr ala
1501/501 1531/511
gtg ggc trg tat gcc cag gac ctc ggc ggc acc acc ggg gtt ccc gtc arg gcc gac gac
val gly leu tyr ala gln asp leu gly gly pro asp gly val pro val met ala asp arg
1561/521
acc ccc cac ccg att gcc asa ccg tga
thr arg his ile ile ala lys pro GPA

SEQ ID N° 19F (suite)

FIGURE 19F (suite)

31/11
CGA GAC ACT GGT GCG GGA CAC TTG AGT TCG GCT GGT AAC GAC GCG AGA GTC GCC CCC TIC
arg asp ser gly ala gly his leu ser ser ala ala ass asp ala arg val ala arg phe
61/21 91/31
CCC GGT GTG GCA CTC ACC TTC GGT GAG GGT ACA CGG GAC CTT CGA GCA CGC ATT ATC GTG
arg val gly leu thr phe gly glu gly thr ala asp leu arg ala arg ass ile val
121/41 151/51
GGC CGG CTG GCA ACC GTC GGT TTC GAC GTT GGT GAC GAC CCC TCG ITC ATG AAT CCT TCT
gly arg leu ala thr val gly phe asp val gly asp asp pro ser phe met asn arg ser
181/61 211/71
TGA CCT CGG CCT TTT CCT GGA TGC CCA CGC ACC GCG GGT ACT GGT GCG CTT AAG CTT CTC
GPA ala pro arg phe ala gly cys pro gly thr ala gly thr ala ala leu lys leu val
241/81 271/91
GGA CAT GGT GCG GGC AGG GAG GAA CAG TGG GCA AGC AGC TAG CGG CGG TCG CGG CGN TCG
ala his gly ala gly arg glu glu gln trp ala ser ser AMB pro arg ser pro arg trp
301/101 331/111
TGG CTG CCT GCA TGC TCG CAG CGG DAT GCA CTC AGC TGG TCG AGG GCA CGG CGG TCG CTC
ser val arg ala cys ser gln pro asp ala pro thr trp ser thr gly pro pro trp leu
361/121
CCG ACA ATX CCG GAC CAC TGG ATT AGG ATC
pro thr ass pro asp his cys ile arg ile

SEQ ID N° 20A

FEUILLE DE REMPLACEMENT (REGLE 26)
FIGURE 20A

74/185

32/11

GAG ACA GTC CTC CGG GAC ACT TGA GTT CGG CTC ACG ACG CCA GAG TCG CGG GCT TCG
 glu thr val val arg asp thr OPA val arg leu leu the thr pro glu ser pro ala ser
 62/21 92/31

GGG GTG TGG GAC TCA CGT TCG GTG AGG GTA CAG CGG ACC TTC GAG CAC GCA ATA TCG TCG
 ala val trp asp ser arg val arg val gln arg thr the phe glu his ala ile ser tip
 122/41 152/51

GCC GGC TGG CAA CGG TCG GTT TCG ACG TTS GTG AGG ACC CCT CCT TCA TGA ATC GTT CTT
 ala gly trp gln pro ser val ser thr leu val thr the pro arg ser OPA ile val leu
 182/61 212/71

GAG CTC CCC GTT TTG CTG GAT GCC CAG GCA CGG GCA GTT CTG CGG TTA AGC TTG TCG
 glu leu pro val leu leu asp ala gln ala pro pro val leu leu arg leu ser leu ser
 242/81 272/91

CAC ATG GTG CGG GCA GGG AGG AAC AGT GGG CAA GCA GCT AGC CGG CCT CGC CGC GCT GGT
 his met val pro ala gly arg asn ser gln gln ala ala ser arg ala arg arg ala gly
 302/101 332/111

CGG TGU GTG CAT GCT CGC AGG CGG ATG CAC CAA CGT GGT CGA CGG GAC CGC CGT GGC TGC
 arg cys val his ala arg ser arg met his gln arg gly arg arg esp arg arg gly cys
 382/121

CGA CAA ATC CGG ACC ACT GCA TCA GGA TC
 arg gln ala arg thr thr ala ser gly

SEQ ID N° 208

FIGURE 208

33/11

AGA CAG TGG TGC GGG ACA CTT GAG TTC GGC TGC TAA CGA CGC CAG AGT CGC CGG CTT CGG
 arg gln trp cys gly thr leu gln phe gly sys OCH ser arg gln ser arg pro leu pro
 63/21 93/31

CGG TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC CGG CCT TCG AGC ATG CAA TAT GGT CGG
 arg cys gly thr his val arg OPA gly tyr ser arg ser ser thr gln tyr arg gly
 123/41 153/51

CGG GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CGG CTC GTT CAT GAA TCG TTC TTG
 pro ala gly asn arg arg phe arg arg trp OPA arg pro leu val his gln ser phe leu
 193/61 213/71

AGC TCC CGG TTT TGC TGG ATG CGG AAC AGG CAC CGC CGG TAC TGC TGC GCT TAA GCT TGT CGC
 ser ser pro phe cys trp met pro arg his arg arg tyro cys cys als OCH als cys arg
 243/81 273/91

ACA TGG TGC CGG CAG GGA GCA AAG GTG GGG AAG CGG CTC ACG GCG CGG CGG CGT CGC
 thr trp cys arg gln gln gly thr val gly lys gln leu als als als als als val
 303/101 333/111

GCT CGG TGG ATG CTC CGA CGC GGA TGC AGC AAC ATG GTG GTC GAC CGG AGC CGC CGT GGT GGC
 gly als cys met leu als als gly cys thr asn val val esp gly thr als val als als
 343/121

GAC AAA TCC CGA CGA CGT CGT CAT CGG GAT C
 asp lys asn gln phe leu his gln esp

SEQ ID N° 209

FEUILLE DE REMPLACEMENT (RÈGLE 26)

75/185

partie de la séquence nucléotidique de seq20A

1/1

31/11

TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC GGA CCT TCG AGC CAA TAT CGT GGG CGG
 cys gly thr his val asp CPA gly tyr ser gly pro ser ser thr gin tyr arg gly pro
 61/21 91/31

GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CUC CTC GTC GTT CAT GAA TCG TTC TTG AGC
 ala gly asn arg arg tyg phe arg arg trp CPA arg pro leu val his glu ser phe leu ser
 121/41 151/51

TCU CCG TTT TGC TGG CCC AGG CAC CGC CGG TAC TGC TCG CCT TAA GCT TGT CGC ACA
 ser pro phe cys trp met pro arg his arg arg tyr cys cys ala OCH ala vty arg thr
 181/61 211/71

TGG TGC CGG CAG GGA GGA ACA GTG GGG AAG CAG CTA CGC CGC CTC CGC CGC CGT CGC CGT
 trp cys arg gin gly gly thr val gly lys gin ile ala ala leu ala als leu val gly
 241/81 271/91

GCG TGC ATG CTC GCA GCC GGA TGC ACC AAC GTC GTC GAC CGC CGC GCT GCT GCG GAC
 ala cys mett leu ala ala gly cys thr asn val val asp gly thr ala val als als als asp
 301/101

AAA TCC CGA CCA CTG CAT CAG GAT C
 lys ser gly pro leu his gln asp

SEQ ID N° 20A'

FIGURE 20A'

1/1

31/11

GTG GGA CTC ACG TTC GCT GAG GGT ACA GCG GAC CTT CGA GCA CGC AAT ATC GTC GGC CGS
 val gly leu thr phe gly gln gly thr als asp leu arg als arg asn ile val gly arg
 61/21 91/31

CTG GCA AAC ATC GGT TTC TCC GAC GTT GGT GAC GAC GCG TGG TTT ATG AAT CGT TCT TGA CGT
 leu ala thr val gly phe asp val gly asp asp pro ser phe met asn arg ser CPA als
 121/41 151/51

CCC CGT TTT CCT GGA TGC CGA CGC ACC GCG GGT ATC GCT GGT GCG CTT AAG CTT GTC GCA CGT
 pro arg phe ala gly cys pro gly thr als gly thr als als leu lys leu val als his
 181/61 211/71

GGT GGC GGC AGG GAG GAA CAG TGG GCA AGC TAG CGG CGC TGG CGG CGC TGG TCG GTC GTC
 gly als als gly arg gln glu trp als ser ser ARG pro arg arg ser pro arg trp ser val
 241/81 271/91

CGT GCA TGC TCG CAA CGG GAT GCA CCA AGC TGG TCG AGC GCA CGG CGC CGG TGG CGT CGC ACA
 arg als cys ser gln pro asp als pro thr trp ser thr gly pro pro trp leu pro thr
 301/101

AAT CGG GAC GAC TGC ATC AGG ATC
 asn pro arg his cys ile arg ile

SEQ ID N° 20B'

FIGURE 20B'

76/185

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L1          31/11
GTC TGG GAC TCA CGT TCG GTG AGG GIA CAG CGG ACC TTC GAG CAC GCA ATA TGT TGG GGC
val trp asp ser arg ser val arg val gln arg thr phe glu his ala ile ser trp ala
61/81      91/731
GCG TGG CAA CGC TCG GTT TCG AGG TTG GTG AGC ACC CCT GCT TCA TGA ATC GTT CTT GAG
gly trp gln pro ser val ser thr leu val tht the pro arg ser CEA ile val leu glu
121/41     181/5)
CTC CCC GTT TTG CTG GAT CGC CAG GCA CGG CGG GIA CTC CGG CGC TGA ACC TTG TGG GAC
cys val pro val leu ala asp ala gln ala pro val val leu leu ala arg leu ser leu
181/61      211/731
TGT GTG CGG GCA CGG AGG AAC ATT TGG GAG CGA CCT AGC CSC GCT CGG CGC CCT GGT CGT
met val pro ala gly arg asn met ser gly gln ala ala ser arg ala arg arg ala gly arg
241/81      271/931
TGC GTG GAT GCT CGC AGC CGG ATG CGC CAA CGT GGT CGA CGC GAG CGC CCT GGC TGA CGA
cys val his ala arg ser arg met his gln arg gly arg arg asp arg arg gly cys arg
361/101
CAA ATC CGG AGC ACT GCA TCA GGA TC
sin ile are the thr ala ser ala

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SEO in N° 20C3

FIGURE 20C*

sequence Pv3176 prédicté par Cole et al. (Nature 303:817-819) et contenant également 1/1
 atg ggc aag cag cta gco ggg ott gco ggg ctg gtc ggt tgg tgg atg ott gca gco ggg
 met gly lys glu leu ala ala leu ala leu val gly ala cys met leu ala ala gly
 61/21 91/31
 tgg acc aac gtc gac gao ggg acc gco ggg gct gac gac met tcc gaa cca ctg car cag
 cys thr amn val val asp gly thr ala val ala ala asp try ser gly pro leu his gln
 121/41 151/53
 gat cgg ata ccc gat tcc ggg ott gac egg ott ctc gac ttg aac cag atc aat gcc
 asp pro ile pro val ser ala leu glu gly leu leu leu asp leu ser gln ile asn ala
 181/61 211/71
 ggg ctg gtt ggg aca tcc att aag gtt ggg ttc aat gac aag gca aat try pac try aag
 ala leu gly ala thr ser met lys val tri phe phe asn ala lys ala met trip asp try aat
 241/81 271/91
 aag aac gtc gac gac aac aat tgn ctc gct att gac gat gca gca ccc gaa ccc gaa aag gtc tat
 lys ser val ala asp lys amn cys leu ala 116 asp gly pro ala gln gln lys val tyr
 301/101 331/111
 gca ggc acc ggg agg acc gct att aag cgg ggc cca cgg ctg gac gac aag aat gat gac tcc
 ala ala gly thr gly trp the ala met arg gly gln arg leu asp asp ser lle asp asp ser
 361/121 391/131
 aac aas ccc gac cac tcc gco att cca ggg gtc gtc aac tcc ccc aac gca cat gat gca
 lys arg asp his tyr ala lle gln ala 181 val gly phe pro the ala his asp ala
 421/161 451/181
 ggg gag ttc the tcc age tec tcc tgg ccc aac age tgg age age tgg tgg age aac ccc egg att gac
 glu glu phe tyc ser ser ser val val ser ser tgg ser ser cys ser arg arg phe val
 481/181 511/191
 gaa ptc acc ccc pga cag gac gac gac gco gco tgg act gng aat gac gac gtr pro san gsc san
 glu val thr pro gly gln asp asp ala ala trp thr val ala asp val val san esp san
 571/191
 ggg aag ccc aac age tec tcc tgg gtt ccc gca ggg aac gga tag age tgg age asp age gca
 gcy met leu ser ser ser gln val gln glu phe gly asp gly trp thr cys gln arg ala
 601/201 631/211
 ctg aat gac gac aac aac gtc acc aac gac act gtc act tgg gac tat aac gac ccc gac gat
 leu thr ala arg san amn val tmr ala asp gln val val val cys ser gln pro esp
 661/221 691/231
 tgg gtt ggg att gtc aat gtc aac ccc aac aac gtc acc aac gac act gtc act tgg gac tat aac gac gat
 leu val ala ala gln ala ala gln ala ala lys val ala ala lys gln AMR

SEQ ID N° 29B

FIGURE 20D

FEUILLE DE REMplacement (RÈGLE 26)